

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 16, 2005, 04:40:32 ; Search time 5885 Seconds
(without alignments)
3451.955 Million cell updates/sec

Title: US-09-939-483-5

Perfect score: 2105

Sequence: 1 ENVRTALIVCTFTYLLVGA.....STGLHSLAFLGLMKRRSSV 405

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US0939483/runat_15092005_111359_9696/app_query.fasta_1.583
-DB=GenEmbl -OPMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=spt -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US0939483.CGN 1 1 4200 @runat_15092005_111359_9696 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAEXT=0.5 -FGAPOP=6
-FGAEXT=7 -YGAPOP=10 -YGAEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*

1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2094.5	99.5	1887	10 AF006824	Mus muscu
2	2090.5	99.3	1888	10 AB008537	Mus muscu
3	2090.5	99.3	2009	10 AB013345	Mus muscu
4	2090.5	99.3	2031	10 AF065162	Mus muscu

5	2065.5	98.1	2077	10 AF031384	AF031384 Rattus no
6	1944	92.4	1324	10 AB048823	AB048823 Rattus no
7	1876	89.1	1313	10 AB048824	AB048824 Rattus no
8	1819	86.4	1551	6 BD222722	BD222722 Human sig
9	1819	86.4	2514	6 AR175708	AR175708 Sequence
10	1819	86.4	2590	9 AF006823	AF006823 Homo sapi
11	1819	86.4	2590	9 AF065163	AF065163 Homo sapi
12	1793	85.2	2588	6 CQ719208	CQ719208 Sequence
13	1642.5	78.0	2574	10 AF242508S2	AF242508 Mus muscu
14	1642.5	78.0	143074	2 AC102222	AC102222 Mus muscu
15	1642.5	78.0	258789	8 AC105298	AC105298 Mus muscu
16	1642.5	76.6	238665	2 AC110465	AC110465 Rattus no
17	1507.5	71.6	897	10 AF022821	AF022821 Mus muscu
18	1422	67.6	956	6 AX224570	AX224570 Sequence
19	1415	67.2	183769	2 AC150884	AC150884 Bos tauru
20	1378	65.5	176625	9 AC015977	AC015977 Homo sapi
21	1326	63.0	854	6 AX181698	AX181698 Sequence
22	1123	53.3	2342	5 BC082937	BC082937 Xenopus 1
23	1102	52.4	82855	5 BX470123	BX470123 Zebrafish
24	1100	52.3	1122	6 AX407227	AX407227 Sequence
25	1100	52.3	1125	6 BD274998	BD274998 Novel Com
26	1100	52.3	1125	6 CQ720250	CQ720250 Sequence
27	1100	52.3	1125	6 AX035342	AX035342 Sequence
28	1100	52.3	1125	6 AX249948	AX249948 Sequence
29	1100	52.3	1125	9 AF212829	AF212829 Homo sapi
30	1100	52.3	1125	9 AF279809	AF279809 Homo sapi
31	1100	52.3	1125	9 AY190605	AY190605 Homo sapi
32	1100	52.3	1206	9 BC075079	BC075079 Homo sapi
33	1100	52.3	1206	9 BC075080	BC075080 Homo sapi
34	1100	52.3	1245	9 AF257080	AF257080 Homo sapi
35	1100	52.3	1248	6 AX302022	AX302022 Sequence
36	1100	52.3	1262	6 AX407225	AX407225 Sequence
37	1100	52.3	1441	6 BD274999	BD274999 Novel Com
38	1100	52.3	1441	6 AX035344	AX035344 Sequence
39	1100	52.3	1441	9 AF248241	AF248241 Homo sapi
40	1100	52.3	2312	6 AX249951	AX249951 Sequence
41	1062.5	50.5	1158	10 AF212827	AF212827 Cavia por
42	994	47.2	1191	10 AF391084	AF391084 Rattus no
43	961.5	45.7	153573	5 BX322589	BX322589 Zebrafish
44	955.5	45.4	1620	10 AF192366	AF192366 Rattus no
45	909	43.2	716	10 AF257082	AF257082 Rattus no

ALIGNMENTS

RESULT 1	AF006824	Mus musculus TWIK-related acid-sensitive K+ channel (TASK) mRNA,	1887 bp	linear	ROD 06-OCT-1997
LOCUS	AF006824	Mus musculus TWIK-related acid-sensitive K+ channel (TASK) mRNA,	1887 bp	linear	ROD 06-OCT-1997
DEFINITION	AF006824	Mus musculus TWIK-related acid-sensitive K+ channel (TASK) mRNA,	1887 bp	linear	ROD 06-OCT-1997
ACCESSION	AF006824	Mus musculus TWIK-related acid-sensitive K+ channel (TASK) mRNA,	1887 bp	linear	ROD 06-OCT-1997
VERSION	AF006824.1	GI:2465543			
KEYWORDS					
SOURCE		Mus musculus (house mouse)			
ORGANISM		Mus musculus			
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS		1 (bases 1 to 1887)			
		Duprat, F., Lesage, F., Fink, M., Reyes, R., Heurteaux, C. and Lazdunski, M.			
TITLE		TASK, a human background K+ channel to sense external pH variations near physiological pH			
JOURNAL		EMBO J. 16 (17), 5464-5471 (1997)			
MEDLINE		97459932			
PUBMED		9312005			
REFERENCE		2 (bases 1 to 1887)			
AUTHORS		Duprat, F., Lesage, F., Fink, M., Reyes, R., Heurteaux, C. and Lazdunski, M.			
TITLE		Direct Submission			
JOURNAL		Submitted (05-JUN-1997) IMPC, CNRS, 660 Route des Lucioles, Sophia-Antipolis, Valbonne 06560, France			
FEATURES		Location/Qualifiers			
		source			
		1..1887			

```
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
<1..1887
/gene="TASK"
<1..1221
/gene="TASK"
/notes="pore-forming K+ channel subunit"
/codon_start=1
/product="TWIK-related acid-sensitive K+ channel"
/protein_id="AAC53367.1"
/db_xref="GI:2465544"
translation="ENVRTIALIVCTFTYLLVGAAPDALESEPMIERORLELRLE
LRARYNISEGYSRELEBRVLRKPKHAGVQVRPAGSPYPAITVITTTIGYGHAAAPSTDG
KQVCFEYALGILPLTLMFQSLGERINTFVRLHRAKRLGNRAHVAESWANNVLIG
FVSCISLTCGAAPSYERYFTFQAYITCITLITITFGDIYVALQDQALQTPQIV
AFSPVYLTGLTVTGAFNLNVLVRFMTNMAEDKRAHRLALITNGQAVLGLGLSCL
SGSLGDIVRPRDPVTCAAAGVGVGSGFRNVAEVLHFQSMSCSLWYKREKIQ
YSIPMIIPDLSTSDTCVEHSHSPGGGGRYSOTPSHPCLCSGTQRSIASSVSTGLHS
LAAFRGLMKRRSSV"
ORIGIN
Alignment Scores:
Pred. No.: 1.46e-172 Length: 1887
Score: 2094.50 Matches: 405
Percent Similarity: 99.75% Conservative: 0
Best Local Similarity: 99.75% Mismatches: 0
Query Match: 99.50% Indels: 1
DB: 10 Gaps: 1
US-09-939-483-5 (1-405) x AF006824 (1-1887)
Qy 1 GluAsnValArgThrLeuAlaLeuValCysThrPheThrTyrLeuValGlyAla 20
Db 1 GAGAAATGTGGCGACGTTGGCTCTCATCGTGGACCTTCACCTACCTGGTGGGCGCC 60
Qy 21 AlaValPheAspAlaLeuGluSerGluProGluMetIleGluArgGlnArgLeuGluLeu 40
Db 61 GCGGTGTTGACGCGACTGGAGTCGGAGCGGAGATGATCGAGCGGACGGCTGGAGCTG 120
Qy 41 ArgGlnLeuGluLeuArgAlaArgTyrAsnLeuSerGluGlyGlyTyrGluGluLeuGlu 60
Db 121 CGGCGAGCTGGAGCTGCGGGCGCGCTACAACTCAGCGAGGCGGCTACGAGGAGCTGGAG 180
Qy 61 ArgValValLeuArgLeuLysProHisValGlyValGlnTyrArgPheAlaGlySer 80
Db 181 CGCGTGTGCTGGCGCTCAAGCCGCAAGCGCGGCTGGAGTGGCGCTTCGCGGCTCC 240
Qy 81 PheTyrPheAlaIleThrValIleThrThrIleGlyTyrGlyHisAlaAlaProSerThr 100
Db 241 TTCTACTTCGCCATCACCGTCATCACCACTCGGCTATGCTATGTCATGCGCGCCAGACG 300
Qy 101 AspGlyGlyLysValPheCysMetPheTyrAlaLeuLeuGlyIleProLeuThrLeuIle 120
Db 301 GACGAGGCAAGGTGTTCTGATGTTCTAGCGCTGTGGGCATCCGCTCACACTAATC 360
Qy 121 MetPheGlnSerLeuGlyGluArgIleAsnThrPheValArgTyrLeuLeuHisArgAla 140
Db 361 ATGTTTCAGAGCCCTGGGTGAACGATCAACACCTTCGTGAGGTACCTGCTGCACCGGCC 420
Qy 141 LysArgGlyLeuGlyMetArgHisAlaGluValSerMetAlaAsnMetValLeuIleGly 160
Db 421 AAGAGGGGCTGGCATGCGGCACCGGAGGTGTCATGGCCACATGTTGCTCATCGT 480
Qy 161 PheValSerCysIleSerThrLeuCysIleGlyAlaAlaPheSerTyrTyrGluArg 180
Db 481 TTCGTGTGTCATCAGCAGCGCTGTCATCGCGCAGCTGCTTCTCTACTACGAGCGC 540
Qy 181 TriThrPhePheGlnAlaTyrTyrCysPheIleThrLeuThrIleGlyPheGly 200
Db 541 TGGACTTCTTCCAGGCTATTACTACTGCTTCATCACCTCCACCATCGGCTTCGGC 600
Qy 201 AspTyrValAlaLeuGlnLysAspGlnAlaLeuGlnThrGlnProGlnTyrValAlaPhe 220
601 GACTATGTGGCGCTGCAGAAGGACCGAGCGCTGCAGACCGCAGCGATATGTGGCCTTC 660
221 SerPheValTyrIleLeuThrGlyLeuThrValIleGlyAlaPheLeuAsnLeuValVal 240
661 AGCTTCGTGTACATCTCTCACGGGCTCACGCGTATCGGCGCTTCTCTCAACCTCGTGTG 720
241 LeuArgPheMetThrMetAsnAlaGluAspGluLysArgAspAlaGluHisArgAlaLeu 260
721 CTGCGATTTCATGACCATGACCGCGGAGGACGAGAGCGTATGCGGAGACCGGCGCTG 780
261 LeuThrHisAsnGlyGlnAlaValGlyLeuGlyGlyLeuSerCysLeuSerGlySerLeu 280
781 CTCACGCACAAACGCCAGGCTGTCGCGCTGGTGGCTGAGCTGCTGAGCGGTAGCCTG 840
281 GlyAsp---ValArgProArgAspProValThrCysAlaAlaAlaGlyGlyValGly 299
841 GGCAGCGGCGTGGCTGCTCCCGCAGCCAGTCACATGCGCTGCGGCGCGGAGGCGTGGC 900
300 ValGlyValGlyGlySerGlyPheArgAsnValTyrAlaGluValLeuHisPheGlnSer 319
901 GTGGCGTGTGGTGGCGCGCTTCCGCAAGCTCTATGCCGAGGTGTGCACCTTCCAGTCC 960
320 MetCysSerCysLeuTyrTyrLysSerArgGluLysLeuGlnTyrSerIleProMetIle 339
961 ATGTGCTGTGGCTCTGTGTACAGAGCGCGGAGAGCTGCAGTACTCCATCCCATGATC 1020
340 IleProArgAspLeuSerThrSerAspThrCysValGluHisSerHisSerProGly 359
1021 ATCCCGCGGACCTCTCCAGTCCGACACCTGCGGTGAGACACAGCCACTCGTCCGCGGA 1080
360 GlyGlyGlyArgTyrSerAspThrProSerHisProCysLeuCysSerGlyThrGlnArg 379
1081 GCGCGGCGCGCTGACAGGACACGCTCACACCTGCTGCTGAGCGGAGCGGCGCGC 1140
380 SerAlaIleSerSerValSerThrGlyLeuHisSerLeuAlaAlaPheArgGlyLeuMet 399
1141 TCGGCCATCAGCTCGGTGTCCAGCGCTGCACAGCTGCTGCTTCCGCGGCTCATG 1200
400 LysArgArgSerSerVal 405
1201 AAGCGAGGAGCTCGGTG 1218
RESULT 2
AB008537
LOCUS Mus musculus mRNA for cTBAK, complete cds. 1888 bp mRNA linear ROD 13-FEB-1999
DEFINITION AB008537
ACCESSION AB008537.1 GI:3043543
VERSION cTBAK.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (sites)
AUTHORS Kim,D., Fujita,A., Horio,Y. and Kurachi,Y.
TITLE Cloning and functional expression of a novel cardiac two-pore
JOURNAL background K+ channel (cTBAK-1)
MEDLINE Circ. Res. 82 (4), 513-518 (1998)
PUBMED 98165556
REFERENCE 2 (bases 1 to 1888)
AUTHORS Fujita,A., Horio,Y. and Kim,D.
TITLE Direct Submission
JOURNAL Submitted (29-OCT-1997) Akikazu Fujita, Osaka University, Faculty
of Medicine, Department of Pharmacology II, Yamada-oka 2-2, Suita,
Osaka 565, Japan (E-mail:afujita@med.id.yamagata-u.ac.jp,
Tel:81-6-879-3512, Fax:81-6-879-3519)
COMMENT On Apr 10, 1998 this sequence version replaced gi:2589004.
Sequence updated (07-Apr-1998).
FEATURES
Location/Qualifiers
source 1..1888
/organism="Mus musculus"
```

gene	/mol_type="mRNA" /db_xref="taxon:10090" /tissue_type="heart" 1. .1888 /gene="mctbak"	
CDS	14. .1243 /gene="mctbak" /codon_start=1 /product="CTBAK" /protein_id="BAA25436.1" /db_xref="GI:3043544" /translation="MKRONVPTALILVCTFYLLVGAAPFDALSEPEMLERQPLELR QLELRARYNLSSGGVEELERVVLRLLKPKHAGQVQWRPAGSFYFALIVITTYIGHAAPS TDGKVCFCMFYALLGIPFTLVNMFQSLGERINTFYVLRLLKRAKGLGRHRAEVSNNVY LTGFCISLTICGAAAFSYERMTFFQAYYYCTFTTIFGFDYVALQDQALQTOP QYVAFSVFVLTGLTVIGAFLLVLRVFWMAEDKRADEHRAALLTHNGOAVGLGL SCLSGSLGSDVPRPDPTCAAAGGVGVGSGSPRNYYAEVLHFSQMSCLWYKSP KLOYSTPMLIPDLSTSDTCVZSHSSPGGGRRYSDTFSHPCLSGTQSRSAISSVSTG LHSLAAFRGLMKRRSSV" 1888 /gene="mctbak" /note="15 A nucleotides"	
polyA_site		
ORIGIN		
Alignment Scores:		
Pred. No.:	3.25e-172	Length: 1888
Score:	2090.50	Matches: 403
Percent Similarity:	99.75%	Conservative: 2
Best Local Similarity:	99.26%	Mismatches: 0
Query Match:	99.31%	Indels: 1
DB:	10	Gaps: 1
US-09-939-483-5 (1-405) x AB008537 (1-1888)		
Qy	1	GlusnValArgThrLeuAlaLeuValCysThrPheThrTyrrLeuLeuValGlyAla 20
Db	23	CAGATGTGGCAGCTGGCTCTCAFCGTGTGCACCTTACACCTACCTGCTGGTGGGCGCC 82
Qy	21	AlaValPheAspAlaLeuGluSerGluProGluMetIleGluAtrGlnArgLeuGluLeu 40
Db	83	CGCGTGTTCAGCCACTGGAGTCGGAGCCGGAGATGATCGAGCGCAGCGCTGGAGCTG 142
Qy	41	ArgGlnLeuGluLeuArgAlaArgfyrAenLeuSerGluGlyGlyTyrrGluGluLeuGlu 60
Db	143	CGCAGCTGGAGCTGGCGGCGCTACAACTCAGCGAGGGCGGCTACGAGGAGCTGGAG 202
Qy	61	ArgValValLeuArgLeuLysProHisLysAlaGlyValGlnTrpArgPheAlaGlySer 80
Db	203	CGCGTGTGTCGGCTCAAGCGCGCAACAAGCGCGGCTGCAATGGCGCTTCGCGCGCTCC 262
Qy	81	PheTyrrPheAlaIleThrValIleThrThrIleGlyTyrrGlyHisAlaAlaProSerThr 100
Db	263	TTCTACTTCCCATCACCCTCATCCACCATCCGCTATGTCATGTCGCGCGCCGAGCAG 322
Qy	101	AspGlyGlyLysValPheCysMetPheTyrrAlaLeuLeuGlyIleProLeuThrIleuile 120
Db	323	GACGGAGGCAAGGTGTTCTCATGTTCTACGCGCTGCTGGGCATCCCGCTCACACTAGTC 382
Qy	121	MetPheGlnSerLeuGlyGluArgIleAenThrPheValArgTyrrLeuLeuHiArgAla 140
Db	383	ATGTTTCAGAGCCTGGGCTGAACGCAATCAACACTTTCGTGAGGTACTCTGTCGACCGCTGCC 442
Qy	141	LysArgGlyLeuGlyMetArgHisAlaGluValSerMetAlaAenMetValLeuIleGly 160
Db	443	AAGAGGGGGCTGGGCATGCGGCACGCGCGAGGTGTCATCGCCAAATGTCATCATCGGT 502
Qy	161	PheValSerCysIleSerThrLeuCysIleGlyAlaAlaAalaphSerTyrrGluArg 180
Db	503	TTCTGTGTGTCATCAGCAGCTGTGCATCGGCGCAGCTGCCTTCTCCTACTACGAGCGC 562
Qy	181	TrpThrPhePheGlnAlaTyrrTyrrCysPheIleThrLeuThrThrIleGlyPheGly 200
Db	563	TGACATTCTTCAGGCTATTACTACTGCTTCATCACCCTCACCCTCACCCTCAGCTCGGCTCGGC 622

```
/codon_start=1
/product="cTBAK"
/protein_id="BAA28349.1"
/db_xref="GI:3149959"
/translation="MKRQNVKTLALIVCTFTYLLVGAADFALSEPEMTERQRLER
QLELRARYNLSEGGYELERVLRLKPKHAGVQWRFGASFYFAITVITTTIGYHAAPS
TDGKFCMFYALGILPLTLVMOFSLGERINTFVYLLHRAKRLGMRHAEVSMANV
LIGFVSCISTLCIGAAAFSVYERWTFQAYYCFITLTTIGFDYVALQKDALOTOP
QYAFSFWYLLTGTVTIGAFNLVLRFTMTNAEDEKRAEHRALLTHNGOAVLGLGL
SCLSGSLDGVRRPDPVTCRAAAGGVGVGGSGFRNVYAEVLHFSQMSCLWYKSRG
KLQYSIMPIPRDUSTDTCVEHSHSPGGGRYSDFPSHPLCSGTQRSIAISSVSTG
LHSLAARGLMKRRSSV"
2009
polyA_site
/note="15 A nucleotides"

ORIGIN
Alignment Scores:
Pred. No.:      3,52e-172      Length:      2009
Score:          2090.50        Matches:      403
Percent Similarity: 99.75%      Conservative: 2
Best Local Similarity: 99.26%      Mismatches: 0
Query Match:      99.31%      Indels:      1
DB:              1.0          Gaps:      1

US-09-939-483-5 (1-405) x AB013345 (1-2009)

Qy      1  GluAenValArgThrLeuAlaLeuIleValCysThrPheThrTyrLeuLeuValGlyAla 20
Db      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
145  CAGAAATGTCGCACGTTGGCTCTCATGTGTGCACCTTCACCTACCTGCTGGTGGGGGCC 204
Qy      21 AlaValPheAspAlaLeuGluSerGluProGluMetIleGluArgGlnArgLeuGluLeu 40
Db      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
205  GCGGTGTTTCGACGCACTGGAGTCGAGCGCGAGATGATCGAGCGCGAGCGCTGAGCTG 264
Qy      41 ArgGlnLeuGluLeuArgAlaArgTyrAsnLeuSerGluGlyGlyTyrGluGluLeuGlu 60
Db      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
265  CGGCAGCTGGAGCTGCGGCGCGCTACAACTCAGCAGGCGCGCTACGAGGAGCTGGAG 324
Qy      61 ArgValValLeuArgLeuLysProHisLysAlaGlyValGlnTrpArgPheAlaGlySer 80
Db      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
325  CGCGTGTGCTGCGCCTCAAGCCGACAGCGCGCGGTGCGAGTGGCGCTTCGCGCGGTCC 384
Qy      81 PheTyrPheAlaIleThrValIleThrThrIleGlyTyrGlyHisAlaAlaProSerThr 100
Db      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
385  TTCTACTTCGCCCATCCGTCATCACCACCATCGCTATGCTATGCTATCGCGCCCGACAG 444
Qy      101 AspGlyGlyLysValPheCysMetPheTyrAlaLeuLeuGlyIleProLeuThrIleLeu 120
Db      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
445  GACGAGGACAAAGGTGTTCTGCATGTTCTACGCGCTGCTGGGCACTCCGCTCACACTAGT 504
Qy      121 MetPheGlnSerLeuGlyLysArgIleAsnThrPheValArgTyrLeuLeuHisArgAla 140
Db      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
505  ATGTTCCAGACCTTGGGTGAACGATCAACACCTTCGTGAGGTACCTGCTGCACCGTGCC 564
Qy      141 LysArgGlyLeuGlyMetArgHisAlaGluValSerMetAlaAsnMetValLeuIleGly 160
Db      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
565  AAGAGGGGGCTGGGCATGCGGCACGCGAGGTGCTCCATGGCCAAACATGGTCTCATCGT 624
Qy      161 PheValSerCysIleSerThrLeuCysIleGlyAlaAlaPheSerTyrTyrGluArg 180
Db      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
625  TTCGTGTGTCATCAGCAGCGCTGTGATCGCGCAGCTGCTTCCTCTACTACGAGCGC 684
Qy      181 TrpThrPhePheGlnAlaTyrTyrCysPheIleThrLeuThrThrIleGlyPheGly 200
Db      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
585  TGGACTTTCTTCCAGGCGCTATTACTGCTTCATCACCCTCACCAATCGGCTTCGGC 744
Qy      201 AspTyrValAlaLeuGlnLysAspGlnAlaLeuGlnThrGlnProGlnTyrValAlaPhe 220
Db      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
745  GACTATGTGGCGCTGCAGAGGACACGCGCGCTGCAGCGCAGCGCGAGTATGTCGCTTC 804
Qy      221 SerPheValTyrIleLeuThrGlyLeuThrValIleGlyAlaPheLeuAsnLeuValVal 240
Db      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
805  AGCTTCGTGTACATCTCTCACGGGCTCACGGTCACTCGCGCGCTTCTCTCAACCTCGTGT 864
```



```
/protein_id="AAG29339.1"
/db_xref="GI:11093518"
/translation="MKRQNVRLALIVCTFTLLVGA AVFDALSEPEMIRQRLELR
QLELRATNLSGGYVEELRVLRKPKAGQVQWRFAGSFYFAITVTITIGYGHAAPS
TDGKVFQMFVALLIGIPLTVMFOSLGRINTFVRYLLHRAKRGGLGMRHAESVWANNV
LIGFVSCISTICIGAAAFYVERWTFFOAYYCITLTITIGFDYVALQKDALQTOP
QYAFPSFYILTLTVIGAFNLVLVLRFTMNAEDERDAEHRALLTHNGCAVGLGEL
SCLGSLGVRRPDPVTCAAAAGGVGVGSGFRNRYAEVLHFPSMCSCLMYKSR
LKQYSIMIIIPRDLSTDTCEVHSHSPGGGRYSDTPSPHCLSGTQRSAISSVSTG
LHSLAAPERGLMKRRSSV"
```

ORIGIN

```
Alignment Scores:
Pred. No.:      3,56e-172      Length:      2031
Score:          2090.50        Matches:      403
Percent Similarity: 99.75%      Conservative: 2
Best Local Similarity: 99.26%      Mismatches: 0
Query Match:      99.31%      Indels:      1
DB:              10           Gaps:        1
```

US-09-939-483-5 (1-405) x AF065162 (1-2031)

```
Qy      1  GluAenValArgThrLeuAlaLeuIleValCysThrPheThrTyrLeuLeuValGlyVala 20
Db      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Qy      241 CAGAATGTGGCAGCGTGGCTCTCATCTGTGTGCACCTTCACCTACTCTGCTGGTGGCGGCC 300
Db      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::

Qy      21  AlaValPheAspAlaLeuGluSerGluProGluMetIleGluArgGlnArgLeuGluLeu 40
Db      GCGGTGTTTCGACGCACTGGAGTCGGAGCGCGGAGATGATCGAGCGGCAGCGGCTGGAGCTG 360

Qy      41  ArgGlnLeuGluLeuArgAlaArgTyrAsnLeuSerGluGlyGlyTyrGluGluLeuGlu 60
Db      CGCGAGCTGGAGCTGCGGCGCGCTTACAACCTCAGCGAGGGCGGCTACGAGAGCTGGAG 420

Qy      61  ArgValValLeuArgLeuLysProHsiLysAlaGlyValGlnTyrArgPheAlaGlySer 80
Db      CGCTGTGCTGTGGCTCAGCCGCAAGCGCGCGTGCAGTGGCGCTTCGCCGGCTCC 480

Qy      81  PheTyrPheAlaIleThrValIleThrThrIleGlyTyrGlyHisAlaAlaProSerThr 100
Db      TTCTACTTCGCCCATCACCGTCATCACCACTCGGCTATGTGTCATGCGGCGCCAGCAGC 540

Qy      101 AspGlyGlyLysValPheCysMetPheTyrAlaLeuLeuGlyIleProLeuThrIleIle 120
Db      GACGAGGCAAGGTGTTCTGATGTCTACGCGCTGCTGGGCATCCCGCTCACACTAGTC 600

Qy      121 MetPheGlnSerLeuGlyGluArgIleAsnThrPheValArgTyrLeuLeuHisArgAla 140
Db      ATGTTCCAGAGCTGGGTGAACGCATCAACACCTTCGTGAGGTACTCTGTCACCGTGCC 660

Qy      141 LysArgGlyLeuGlyMetArgHisAlaGluValSerMetAlaAsnMetValLeuIleGly 160
Db      AAGAGGGGGCTGGGATCGGCACGCCGAGGTGTCATGGCCACATGTCGTCTCATCGT 720

Qy      161 PheValSerCysIleSerThrLeuCysIleGlyAlaAlaAlaPheSerTyrTyrGluArg 180
Db      TTCGTGCTGTGCATCAGCAGCGTGTGCATCGCGCAGCTGCTTCTCCTACTACGAGCGC 780

Qy      181 TrpThrPhePheGlnAlaTyrTyrCysPheIleThrLeuThrIleGlyPheGly 200
Db      TGGACTTTCTCCAGGCTATTACTACTGTCTTCATCACCCCTCACCACTCGGCTTCGGC 840

Qy      201 AspTyrValAlaLeuGlnLysAspGlnAlaLeuGlnThrGlnProGlnTyrValAlaPhe 220
Db      GACTATGTGGCGCTGCAGAGGACGAGCGGCTGCAGACGCGCCGACATGTGGCCTTC 900

Qy      221 SerPheValTyrIleLeuThrGlyLeuThrValIleGlyAlaPheLeuAsnLeuValVal 240
Db      AGCTTCGTGTATCATCTCAGCGGCTCATCGGTTCATCGGCGCTTCTCCTCAACCTCGTGTG 960

Qy      241 LeuArgPheMetThrMetAsnAlaGluAspGluLysArgAspAlaGluHisArgAlaLeu 260
Db      CTGCGATTTCATGACCATGAACCGGAGGACGAGAGCGTGTATGCGGAGCACCGGCGCCCTG 1020
```

```
Qy      261 LeuThrHisAenGlyGlnAlaValGlyLeuGlyGlyLeuSerCysLeuSerGlySerLeu 280
Db      CTACGACACACGCCAGGCTGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTG 1080

Qy      281 GlyAsp---ValArgProArgAspProValThrCysAlaAlaAlaAlaGlyGlyValGly 299
Db      GGCACGCGGTGCGTCCCCCGGACCAAGTACATGCGCTGCGCGCGCGGAGGCGTGGGC 1140

Qy      300 ValGlyValGlyGlySerGlyPheArgAsnValTyrAlaGluValLeuHisPheGlnSer 319
Db      GTGGGCGTGGTGGCAGGGGCTTCGGCAACGCTATATGCCGAGGTGCTGCACCTCCAGTCC 1200

Qy      320 MetCysSerCysLeuTyrTyrLysSerArgGluLysLeuGlnTyrSerIleProMetIle 339
Db      ATGTGCTCGTGCCTCTGTGTACAGAGCGCGGAGAGCTGCGAGTACTCCATCCCATGATC 1260

Qy      340 IleProArgPheLeuSerThrSerAspThrCysValGluHisSerHisSerSerProGly 359
Db      ATCCCGCGGGACCTCTCCAGCTCCGACACCTGCGTGGAGCACACGACCTCGTGGCGGGA 1320

Qy      360 GlyGlyGlyArgTyrSerAspThrProSerHisProCysLeuCysSerGlyThrGlnArg 379
Db      GCGCGCGCGCGCTACAGGACACGCGCTCACACCCCTGCTGTGCGAGCGGACGCGCGC 1380

Qy      380 SerAlaIleSerSerValSerThrGlyLeuHisSerLeuAlaAlaPheArgGlyLeuMet 399
Db      TCGGCCATCAGTCGGTGTCCAGCGGCTGCACAGCCTGGCTGCTTCGCGGCGCTCATG 1440

Qy      400 LysArgArgSerSerVal 405
Db      AAGCGCAGGAGCTCGGTG 1458

RESULT 5
LOCUS      AF031384
DEFINITION Rattus norvegicus TWIK-related acid-sensitive K+ channel (TASK)
mRNA, complete cds.
ACCESSION  AF031384
VERSION    AF031384.1 GI:2809390
KEYWORDS   .
SOURCE      Rattus norvegicus (Norway rat)
ORGANISM   Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE  1 (bases 1 to 2077)
AUTHORS   Leonoudakis,D., Gray,A.T., Winegar,B.D., Kindler,C.H., Harada,M.,
            Taylor,D.M., Chavez,R.A., Forsayeth,J.R. and Yost,C.S.
TITLE      An open rectifier potassium channel with two pore domains in tandem
            cloned from rat cerebellum
JOURNAL    J. Neurosci. 18 (3), 868-877 (1998)
MEDLINE    98099797
PUBMED     9437008
REFERENCE  2 (bases 1 to 2077)
AUTHORS   Leonoudakis,D., Gray,A.T., Winegar,B.D., Kindler,C.H., Harada,M.,
            Taylor,D.M., Chavez,R.A., Forsayeth,J.R. and Yost,C.S.
TITLE      Direct Submission
JOURNAL    Submitted (24-OCT-1997) Dept. of Anesthesia, UC San Francisco, 513
            Parnassus Ave., San Francisco, CA 94143-0542, USA
FEATURES   Location/Qualifiers
            source
            1..2077
            /organism="Rattus norvegicus"
            /mol_type="mRNA"
            /db_xref="taxon:10116"
            /tissue_types="cerebellum"
            /dev_stage="adult"
            1..2077
            /gene="TASK"
            104..1339
            /gene="TASK"
            /function="open rectifier potassium channel"
            /function="baseline potassium channel"
```

/note="two tandem pore domains; pH and local anesthetic sensitive"
/codon_start=1
/product="TWIK-related acid-sensitive K+ channel"
/protein_id="AAC39952.1"
/db_xref="GI:2809391"
translation="MKQNVRTTALIVCTFTYLLVGAAPDALESEPEMTERORLEUR
OLEARYNLSGGYELERVLRLKPKHAGVWRPAGSFVFAITVITIGYGAAPS
TDGKVFCEYVALLGIPLTLVMPQSLGERINTFVYLHRAKRLGMRHAEVSNWV
LIGFVSCISILCTICGAAAFSYERWTFQAYYCFITLTTIGFDYVALXQDALQTOP
QYVAFSVYILGLTVTGAFNLVLRVFMNTNABEDKRAEHRALLTHNQAGLGLGL
SCLSGSGIDPRDTPVTCAAAGMGVGVGGSGFRNVAEMLHPQSMCSCLWYS
REKLQYGPIMIIIPRDLSTSDTCEVHSHSPGGGRYSIDTPSHPCLCSGTQRSATSSVS
TGLHSLATFRGLMKRRSSV"

ORIGIN

Alignment Scores:
Pred. NO.: 5.5e-170 Length: 2077
Score: 2065.50 Matches: 400
Percent Similarity: 98.77% Conservative: 3
Best Local Similarity: 98.04% Mismatches: 2
Query Match: 98.12% Indels: 3
DB: 10 Gaps: 2

US-09-939-483-5 (1-405) x AF031384 (1-2077)

Qy	1	GluAsnValArgThrLeuAlaLeuValCysThrPheThrTyrLeuLeuValGlyAla	20
Db	113	CAGAAATGTGGCGAGTGGCTCTCATCGTGGACCTTACCTACCTACCTGGTGGCGCC	172
Qy	21	AlaValPheAspAlaLeuGluSerGluProGluMetIleGluArgGlnArgLeuGluLeu	40
Db	173	GCGETGTTCGAGCGCTGGAGTCGGAGCGGAGATGATCGAGCGGCGCTGGAGCTG	232
Qy	41	ArgGlnLeuGluLeuArgAlaArgTyrAsnLeuSerGluGlyGlyTyrGluGluLeuGlu	60
Db	233	CGGCGAGCTGGAGCTGCGGCGCGCTACAACTCAGCAGGCGCGCTACGAGGAGCTGG	292
Qy	61	ArgValValLeuArgLeuLeuPheHisValGlyValGlnTyrArgPheAlaGlySer	80
Db	293	CGCGTGTGCTGGCGCTCAAGCCCAAGCGCGGCGTGCAGTGGCGCTTCGCGCGCTCC	352
Qy	81	PheTyrPheAlaIleThrValIleThrThrIleGlyTyrGlyHisAlaAlaProSerThr	100
Db	353	TTCTACTTGGCCATCCGCTCATCCACCAATCGCTATGTCATCGCGCTCCCGACAG	412
Qy	101	AspGlyGlyIysValPheCysMetPheTyrAlaLeuLeuGlyIleProLeuThrLeuIle	120
Db	413	GACGAGGCAAGGTGTCTGCTATCTTACGCGCTGCTGGCGCATCCGCTCACACTAGTC	472
Qy	121	MetPheGlnSerLeuGlyGluArgIleAsnThrPheValArgTyrLeuLeuHisArgAla	140
Db	473	ATGTTTCAGAGCCTGGGTGAACGCATCAACACCTTCGTGAGGTACCTGCTGCACCGGCG	532
Qy	141	LysArgGlyLeuGlyMetArgHisAlaGluValSerMetAlaAsnMetValLeuIleGly	160
Db	533	AAGAGGGGCTGGCATCGGCACCGCAGGTGTCATGGCCACATGGTCTCATCGT	592
Qy	161	PheValSerCysIleSerThrLeuCysIleGlyAlaAlaAlaPheSerTyrTyrGluArg	180
Db	593	TTCTGTGCTGCATCAGCAGCGCTGTATCGCGCGCTGCTTCTCTACTATGAGCGC	652
Qy	181	TrpThrPhePheGlnAlaTyrTyrCysPheIleThrLeuThrThrIleGlyPheGly	200
Db	653	TGGACTTCTTCCAGGCTATTACTGCTTTCATCACCTTCACACCATCGGCTTCGGC	712
Qy	201	AspTyrValAlaLeuGlnLysAspGlnAlaLeuGlnThrGlnProGlnTyrValAlaPhe	220
Db	713	GACTACGTGGCGCTGCAGAGGACCGCGCTGCAACCGCAGCGCTCAGTACGTGGCTTC	772
Qy	221	SerPheValTyrIleLeuThrGlyLeuThrValIleGlyAlaPheLeuAsnLeuValVal	240
Db	773	AGCTTCGTATACATCCTCACCGGCTCACGGTTCACGGCTTCTTCTCAACCTCGTGGT	832

Qy	241	LeuArgPheMetThrMetAsnAlaGluAspGluLeuArgAspAlaGluHisArgAlaLeu	260
Db	833	CTCGATTTCATGACCATGAACGCCGAGGACGAGCGTGATGCGAGAGCACCGTGCCTG	892
Qy	261	LeuThrHisAsnGlyGlnAlaValAlaGlyLeuGlyCysLeuSerCysLeuSerGlySerLeu	280
Db	893	CTCAGCGCACAAATGCCAGGCTGGCGGCTGGTGGCTGAGCTGCTTAAGCGGTAGCCTG	952
Qy	281	GlyAsp---ValArgProArgAspProValThrCysAlaAlaAlaAlaGly-----Gly	297
Db	953	GGCGATGGCGTGGCTGCCCGGACCCAGTCACATTGGCGACGCGCTGCAGCGGCATCGGC	1012
Qy	298	ValGlyValGlyValGlyGlySerGlyPheArgAsnValTyrAlaGluValLeuHisPhe	317
Db	1013	GTGGCGTGGCGCTGGTGGCAGCGGCTTCGCAACGTCATGCTGAAATGCTGCACATT	1072
Qy	318	GlnSerMetCysSerCysLeuTyrTyrLysSerArgGluLeuGlnTyrSerIlePro	337
Db	1073	CAGTCCATGTGCTCGTGCCTCTGTTACAGAGCGGAGAGCTGCAGTACTCCATCCCC	1132
Qy	338	MetIleIleProArgAspLeuSerThrSerAspThrCysValGluHisSerHisSerSer	357
Db	1133	ATGATCATCCCGCGGACCTCTCCACATCCGACACGTCGCTGAGGACACGCCACTCGTCG	1192
Qy	358	ProGlyGlyGlyGlyArgTyrSerAspThrProSerHisProCysLeuCysSerGlyThr	377
Db	1193	CAAGAGGCGGCGCGCTACAGGACACGCTTCACACCTTGCCTGCTGCGAGCGGACG	1252
Qy	378	GlnArgSerAlaIleSerSerValSerThrGlyLeuHisSerLeuAlaAlaPheArgGly	397
Db	1253	CAAGCTCGGCCCATCAGTCCGTTGCCAGCGGCTGCACAGCTGCTTCCGCGGC	1312
Qy	398	LeuMetIysArgArgSerSerVal	405
Db	1313	CTCATGAAGCGCAGGAGCTCAGTG	1336
RESULT 6			
AB048823			
LOCUS	AB048823	1324 bp	mRNA linear ROD 14-OCT-2000
DEFINITION	Rattus norvegicus KCNK3b mRNA for TASK1 splice bvariant (TASK1b),		
	complete cds.		
ACCESSION	AB048823		
VERSION	AB048823.1	GI:10801597	
KEYWORDS	Rattus norvegicus (Norway rat)		
SOURCE	Rattus norvegicus		
ORGANISM	Rattus norvegicus		
REFERENCE	1 (sites)		
AUTHORS	Ohya,S., Kitsukawa,M. and Imaizumi,Y.		
TITLE	TASK1 splice bvariant (TASK1b) (KCNK3b)		
JOURNAL	Published Only in DataBase (2000)		
REFERENCE	2 (bases 1 to 1324)		
AUTHORS	Ohya,S., Kitsukawa,M. and Imaizumi,Y.		
TITLE	Direct Submission		
JOURNAL	Submitted (13-SEP-2000) Susumu Ohya, Nagoya City University,		
	Department of Molecular and Cellular Pharmacology; 3-1 Tanabedori,		
	Mizuhoku, Nagoya 4678603, Japan (E-mail:sohya@phar.nagoya-cu.ac.jp,		
	Tel:81-52-8363433, Fax:81-52-8363432)		
FEATURES	Location/Qualifiers		
source	1..1324		
	/organism="Rattus norvegicus"		
	/mol_type="mRNA"		
	/db_xref="taxon:10116"		
	/sex="male"		
	/tissue_type="brain"		
gene	1..1324		
	/gene="KCNK3b"		
CDS	14..1192		
	/gene="KCNK3b"		
	/codon_start=1		


```
/protein_id="BAB16711.1"
/db_xref="GI:10801600"
/translation="MFVALLGILPLTVMFQSLGERINTFYRILLHRAKRGIGMRHAEV
SMANNVLIGFVSCISTICIGAAFSYTERWTFFOAYIYCFILITIGFGDIYVALQKQD
ALQTPQYVAFSPFYIILGTIVTGAFNLVLRPMTNNAEDKRDADHRAALLTHNGQA
GGGLGSLGSLGDGVRPRDPVTTCAAAAGMGVGVGGSGFRNVVAEMLHFQSMGCS
CLWYKSRKQLQYSIPMIIPRDLSTSDTCVEHSHSPGGGGRYSDTPSPHCLCSGTQRS
AIVSVSTGLSLATFRGLMKRRSSV"

ORIGIN
Alignment Scores:
Pred. No.:          9,76e-154      Length:      1313
Score:             1876.00         Matches:      370
Percent Similarity: 91.44%         Conservative:  8
Best Local Similarity: 90.46%      Mismatches:   27
Query Match:       89.12%          Indels:        3
DB:                10              Gaps:         3

US-09-939-483-5 (1-405) x AB048824 (1-1313)

Qy   1  GluAsnValArgThrLeuAlaLeuIleValCysThrPheThrTyrLeuLeuValGlyAla 20
Dy   23 CAGAAATGGCGCAGTGTGGCTCTCATGTGTGCACCTTCACCTACCTGCTGGTGGCGGCC 82
Qy   21 AlaValPheAspAlaLeuGluSerGluProGluMetIleGluArgGlnArgLeuGluLeu 40
Dy   83 GCGGTGTTCGACGGCTCCAG-----
Qy   41 ArgGlnLeuGluLeuArgAlaArgTyrAsnLeuSerGluGlyGlyTyrGluGlu-LeuG1 60
Dy   104 -----CTCTCGTAGCGCGCCCTCGCTGAGGTGGGA 133
Qy   60 uArgValValLeuArgLeuLysProHisLysAlaGlyValGlnTrpArgPheAlaGlySe 80
Dy   134 GCGCGTGTGCTGCGCTCAAGCGCACAAAGCGCGCGTGCAGTGGCGCTTCGCGCGCTC 193
Qy   80 rPheTyrPheAlaIleThrValIleThrThrIleGlyTyrGlyHisAlaAlaProSerTh 100
Dy   194 CTCTACTTCGCCATCACCCTCATCACACATCGGTATGGTATGTCATCGGGCTCCACGAC 253
Qy   100 rAspGlyGlyLysValPheCysMetPheTyrAlaLeuLeuGlyIleProLeuThrLeuI1 120
Dy   254 GGACGGAGGCAAGGTGTTCATGCTTCTACCGCTGCTGGCATCCCGCTTCACACATGT 313
Qy   120 eMetPheGlnSerLeuGlyGluArgIleAsnThrPheValArgTyrLeuLeuHisArgAl 140
Dy   314 CATGTTCCAGAGCTGGGTGAACGCATCAACACCTTCGTGAGGTACCTGTGCACCGTGC 373
Qy   140 aLysArgGlyLeuGlyMetArgHisAlaGluValSerMetAlaAsnMetValLeuIleG1 160
Dy   374 GAAGAGGGGGCTGGGCATCGGCACGCGAGGTGTCCATGGCCAAACATGGTCTCATCGG 433
Qy   160 yPheValSerCysIleSerThrLeuCysIleGlyAlaAlaAlaPheSerTyrTyrGluAr 180
Dy   434 TTTCTGTGTGTGTCATCAGCACGCTGTATCGCGCGCGCTGCCCTTCTCTACTATGAGCG 493
Qy   180 gTTPThrPhePheGlnAlaTyrTyrCysPheIleThrLeuThrIleGlyPheG1 200
Dy   494 CTGACATTTCTTCAGGCGCTATTACTACTGCTTCATCACCTTCACCACTACGCGCTTCGG 553
Qy   200 yAspTyrValAlaLeuGlnLysAspGlnAlaLeuGlnThrGlnProGlnTyrValAlaPh 220
Dy   554 CGACTAGTGGCGCTGCAGAGGAGGACGAGCGCTGCNAACGACGCTCAGTACGTGGCCTT 613
Qy   220 eSerPheValTyrIleLeuThrGlyLeuThrValIleGlyAlaPheLeuAsnLeuValVa 240
Dy   614 CAGCTTGTGTATACATCTCACCGCGCTCAGCGTTCATCGCGCGCTTCCTCAACCTCGTGGT 673
Qy   240 lLeuArgPheMetThrMetAsnAlaGluAspGluLysArgAspAlaGluHisArgAlaLe 260
Dy   674 GCTCGGATTATGACCATGAAACGCGGAGGAGGAGCGGTATGATGACAGGACCGCTGGCT 733
Qy   260 uLeuThrHisAsnGlyGlnAlaValGlyLeuGlyGlyLeuSerCysLeuSerGlySerLe 280
```

ORIGIN		/db_xref="taxon:9606"	
Alignment Scores:			
Pred. No.:	1.1e-148	Length:	1551
Score:	1819.00	Matches:	357
Percent Similarity:	90.37%	Conservative:	9
Best Local Similarity:	88.15%	Mismatches:	25
Query Match:	86.41%	Indels:	14
DB:	6	Gaps:	2
US-09-939-483-5 (1-405) x BD222722 (1-1551)			
Qy	1	GluAenValArgThrLeuAlaLeuileValCysThrPheThrTyrLeuLeuValGlyAla	20
Db	41	CAGAAAGTGGCGACGCTGGCGCTCATCGTGTGCACCTTCCACCTACCTGCTGTGGTGGCGCC	100
Qy	21	AlaValPheAspAlaLeuGluSerGluProGluMetIleGluAtrGlnArgLeuGluLeu	40
Db	101	GGCGTCTTCGACCGCTGGAGTCGGAGCCCGAGCTGATCGAGCGCGAGCTGGAGCTG	160
Qy	41	ArgGlnLeuGluLeuArgAlaArgTyrAenLeuSerGluGlyGlyTyrGluGluLeuGlu	60
Db	161	CGGACGAGGAGCTGGCGCGCGCTACAACTTCAGCCAGGCGCGCTACGAGGAGCTGGAG	220
Qy	61	ArgValValLeuArgLeuLysProHisLysAlaGlyValGlnTrpArgPheAlaGlySer	80
Db	221	CGCGTGTGTGGCTCAAGCGGCACAAAGCGCGCGTGCATGTGGCGCTTCGCGGCTCC	280
Qy	81	PheTyrPheAlaIleThrValIleThrThrIleGlyTyrGlyHisAlaAlaProSerThr	100
Db	281	TTCCTACTTCGCCATCACCCTATCACCATCGCTACGGGCAGCGCGCGCACCGAGCAG	340
Qy	101	AspGlyGlyLysValPheCysMetPheTyrAlaLeuLeuGlyIleProLeuThrLeuIle	120
Db	341	GATGCGCGCAAGGTCTTCGATGTTCTACGCGCTGTCTGGCATCCCGCTCACGCTCGTC	400
Qy	121	MetPheGlnSerLeuGlyGluArgIleAenThrPheValArgTyrLeuLeuHisArgAla	140
Db	401	ATGTTCCAGAGCTGGCGGAGCGCATCAACCTTGTGTGAGTACTCTCTGCACCGCGCC	460
Qy	141	LysArgGlyLeuGlyMetArgHisAlaGluValSerMetAlaAenMetValLeuIleGly	160
Db	461	AAGAAGGGCTGGCGATCGCGCGCGCGCGCGTCCATGGCCCAACATGGTCTCATCGGC	520
Qy	161	PheValSerCysIleSerThrLeuCysIleGlyAlaAlaAlaPheSerTyrTyrGluArg	180
Db	521	TTCCTCTGTGATCAGCAGCTGTGCATCGCGCGCGCGCGCTTCTCCACTACGAGCAC	580
Qy	181	TrpThrPhePheGlnAlaTyrTyrCysPheIleThrLeuThrThrIleGlyPheGly	200
Db	581	TGGACCTTCTTCAGGCGCTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	640
Qy	201	AspTyrValAlaLeuGlnLysAspGlnAlaLeuGlnThrGlnProGlnTyrValAlaPhe	220
Db	641	GACTAGTGGCGCTGCAGAAAGACAGAGCGCTTCGAGACGCGAGCTAGCTGGCGCTTC	700
Qy	221	SerPheValTyrIleLeuThrGlyLeuThrValIleGlyAlaPheLeuAenLeuValVal	240
Db	701	AGCTTCGTCTACATCTTACGGCGCTCAGGTCATCGCGCGCTTCTCTCACTCTGTGGTG	760
Qy	241	LeuArgPheMetThrMetAenAlaGluAspGluLysArgAspAlaGluHisArgAlaLeu	260
Db	761	CTGCGCTTTCATGACATGAACCGGAGGACGAGAGCGCGCGCGAGCACCGCGCGCTG	820
Qy	261	LeuThrHisAenGlyGlnAlaValGlyLeuGlyGlyLeuSerCysLeuSerGlySerLeu	280
Db	821	CTCAGCGCAACGGCG	880
Qy	281	GlyAspValArgProArgAspProValThrCysAlaAlaAlaAlaGlyGlyValGlyVal	300
Db	880	GGCAGCGCGCACACTACGAGCACCGCGCTCATCCAGCGCGGAGCGGCGCGCGCGCG	904

Db 375 TTCTACTCGCCATCATCCGCTCATCACCACTCGCTACGGGCACGGCCACCCAGCACG 434
Qy 101 AspGlyGlyLysValPheCysMetPheTyrAlaLeuLeuGlyIleProLeuThrLeuIle 120
Db 435 GATGGCGCAGAGGTGTTCTGATGTTCTACGCGTGTGGGCATPCCGCTCACGCTCGTC 494
Qy 121 MetPheGlnSerLeuGlyGluArgIleAsnThrPheValArgTyrLeuLeuHisArgAla 140
Db 495 ATGTTCCAGACCTGGCGAGCGCATCAACCTTGTGAGTACCTGCTGCACCGCGCC 554
Qy 141 LysArgGlyLeuGlyMetArgHisAlaGluValSerMetAlaAsnMetValLeuIleGly 160
Db 555 AAGAAGGGCTGGGCATGCGCGCGCGACGAGTGTCCATGGCCAAACATGGTCTCATCGC 614
Qy 161 PheValSerCysIleSerThrLeuCysIleGlyAlaAlaPheSerTyrTyrGluArg 180
Db 615 TTCTTCTCGTGATCAGACGCTGTGATCGCGCGCGCTTCTCCCACTACGAGCAC 674
Qy 181 TrpThrPhePheGlnAlaTyrTyrCysPheIleThrLeuThrThrIleGlyPheGly 200
Db 675 TGGACCTTCTCCAGGCTACTACTACTGCTTCATCACCTCACCACTCGGCTTCGGC 734
Qy 201 AspTyrValAlaLeuGlnLysAspGlnAlaLeuGlnThrGlnProGlnTyrValAlaPhe 220
Db 735 GACTACGTGGCGCTGCAGAGGACAGCGCCCTGCAGACGCGACGCGAGTACGTGGCCTTC 794
Qy 221 SerPheValTyrIleLeuThrGlyLeuThrValIleGlyAlaPheLeuAsnLeuValVal 240
Db 795 AGCTTGTGCTACATCTTACGGGCTCACGCTCATCGCGCTTCTCAACCTCGTGGTG 854
Qy 241 LeuArgPheMetThrMetAsnAlaGluAspGluLysArgAspAlaGluHisArgAlaLeu 260
Db 855 CTGGCGCTTATGACCATGACCGCGAGGACGAGAGCGCGACGCGCGAGCGCGCTG 914
Qy 261 LeuThrHisAsnGlyGlnAlaValGlyLeuGlyLeuSerCysLeuSerGlySerLeu 280
Db 915 CTACGGCGCAACGGCGAGCGCGCGCGCGAGG-----GGT 953
Qy 281 GlyAspValArgProArgAspProValThrCysAlaAlaAlaGlyValGlyVal 300
Db 954 GGCAGCGGCACACTACGACACCGCCTCATCCACGGCGGCGCG----- 998
Qy 301 GlyValGlyGlySerGlyPheArgAsnValTyrAlaGluValLeuHisPheGlnSerMet 320
Db 999 -----GGCGCGCGCGCTCCGCAACGCTACCGCGGGTGTGCACTTCCAGTCCATG 1052
Qy 321 CysSerCysLeuTyrTyrLysSerArgGluLysLeuGlnTyrSerIleProMetIleIle 340
Db 1053 TGCTCGTGCCTGTGTGTCACAGAGCGCGAGAGCTGCAGTACTCCATCCCCCATGATCATC 1112
Qy 341 ProArgPheLeuSerThrSerAspThrCysValGluHisSerHisSerSerProGlyGly 360
Db 1113 CCGCGGACCTCTCCAGTCCGACGCTGCGTGGAGCAGAGCCACTCGTCCCGGGAGGG 1172
Qy 361 GlyGlyArgTyrSerAspThrProSerHisProCysLeuCysSerGlyThrGlnArgSer 380
Db 1173 GCGCGCGCTACAGGACACGCGCTCGCGACGCTGCTGTGACGGGGGCCACGCTCC 1232
Qy 381 AlaIleSerSerValSerThrGlyLeuHisSerLeuAlaAlaPheArgGlyLeuMetLys 400
Db 1233 GCCATCAGCTCGTGTCCACGGGTCTGCACAGCGCTGTCCACCTTCCCGCGGCTCATGAAG 1292
Qy 401 ArgArgSerSerVal 405
Db 1293 CGCAGGAGCTCCGTG 1307

RESULT 10
AF006823
LOCUS AF006823 2590 bp mRNA linear PRI 06-OCT-1997
DEFINITION Homo sapiens TWIK-related acid-sensitive K+ channel (TASK) mRNA,
complete cds.
ACCESSION AF006823
VERSION AF006823.1 GI:2465541

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2590)
AUTHORS Duprat,F., Lesage,F., Fink,M., Reyes,R., Heurteaux,C. and Lazdunski,M.
TITLE TASK, a human background K+ channel to sense external pH variations near physiological pH
JOURNAL EMBO J. 16 (17), 5464-5471 (1997)
MEDLINE 97459932
PUBMED 9312005
REFERENCE 2 (bases 1 to 2590)
AUTHORS Duprat,F., Lesage,F., Fink,M., Reyes,R., Heurteaux,C. and Lazdunski,M.
TITLE Direct Submission
JOURNAL Submitted (05-JUN-1997) IMPC, CNRS, 660 Route des Lucioles, Sophia-Antipolis, Valbonne 06560, France
FEATURES
source Location/Qualifiers
1..2590
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
1..2590
/gene="TASK"
126..1310
/gene="TASK"
/notes="pore-forming K+ channel subunit"
/codon_start=1
/product="TWIK-related acid-sensitive K+ channel"
/protein_id="AAC51777.1"
/db_xref="GI:2465542"
/translation="MKRQNRVTALIVCTFTYLLVGAADVDALESPELLERQRLER QQSLARYNLSSQGGEELERLVRLKPKAGVQMRFAGSYFAITVTITTYGHAAPS TDGKVCVFYALLGIPLTLMFQSLGERINTLYRLHRAKGLGNRRADVSMANNV LIQFGFCISLTCIGAAAFSHYHWTFOAYYCFITLTITFGDYVALQDQALQTP QYVAFSPVILTGLTVIGLFLNLVLRFMTHNAEDKRAEHALLTRNQAGGGGG GSAHTDTASTTAAGGGRPNVYAEVLHFEQSCMLWYKSKLOYSIPMIIPRDL S TSDTCVEQSHSSPGGGGRYSDTFSRRCLCSGAPRSALISSVSTFRLMKRRS SV"
ORIGIN
Alignment Scores:
Pred. No.: 2,09e-148 Length: 2590
Score: 1819.00 Matches: 357
Percent Similarity: 90.37% Conservative: 9
Best Local Similarity: 88.15% Mismatches: 25
Query Match: 86.41% Indels: 14
DB: Gaps: 2
US-09-939-483-5 (1-405) x AF006823 (1-2590)
Qy 1 GluAsnValArgThrLeuAlaLeuIleValCysThrPheThrTyrLeuLeuValGlyAla 20
Db 135 CAGAACGTGCGACGCTGGCGCTCATCGTGTGACCTTACCTACCTGCTGGTGGCGCC 194
Qy 21 AlaValPheAspAlaLeuGluSerGluProGluMetIleGluArgGlnArgLeuLeu 40
Db 195 GCGGTCTTCCACGCGCTGGAGTCGGAGCCGAGCTGATCGAGCGGCGAGCTGGAGCTG 254
Qy 41 ArgGlnLeuGluLeuArgAlaArgTyrAsnLeuSerGluGlyTyrGluGluLeuGlu 60
Db 255 CGGCAGCAGGAGCTGCGGGCGCGCTACAACTCAGCAGCGCGGCTACGAGAGCTGAG 314
Qy 61 ArgValValLeuArgLeuLysProHisLysAlaGlyValGlnTyrArgPheAlaGlySer 80
Db 315 CGCGTCTGCTGCGCTCAAGCGGCACAAGCGCGGCTGCGAGTGGCGCTTTCGCGGCTCC 374
Qy 81 PheTyrPheAlaIleThrValIleThrThrIleGlyTyrGlyHisAlaAlaProSerThr 100
Db 375 TTCTACTTCGCCATCACCGCTCATCACCACTCGCTACGGGCACCGCGCACCCAGCACG 434

Qy 101 AspGlyGlyValPheCysMetPheThrValAlaLeuGlyLeuProLeuThrLeuIle 120
Db 435 GATGCGGCAAGGTTCTTCATGTTCTACGCGCTGGCGCATCCCGCTCACGCTCGTC 494
Qy 121 MetPheGlnSerLeuGlyGluArgIleAsnThrPheValArgTyrLeuLeuHisArgAla 140
Db 495 ATGTTCCAGAGCTGGGAGCGCATCAACACCTTGGTGAGGTACTCTGTCACCGCGCC 554
Qy 141 LysArgGlyLeuGlyMetArgHisAlaGluValSerMetAlaAsnMetValLeuIleGly 160
Db 555 AAGAGGGGCTGGGCATCGCGCGCCGACGTGCTCATGGCAACATGGTCTCATCGGC 614
Qy 161 PheValSerCysIleSerThrLeuCysIleGlyAlaAlaPheSerTyrTyrGluArg 180
Db 615 TTCTTCTCGTCATCAGACGCTGTCATCGCGCGCGCTTCTCCACCATCAGACGAC 674
Qy 181 TrpThrPheGlnAlaTyrTyrCysPheIleThrLeuThrIleGlyPheGly 200
Db 675 TGGACCTTCTTCAGGCTTACTACTGCTTCTCATCCCTCACCATCGGCTTCGGC 734
Qy 201 AspTyrValAlaLeuGlnLysAspGlnAlaLeuGlnThrGlnProGlnTyrValAlaPhe 220
Db 735 GACTACGTGGCGCTGCAGAGGACGAGCGCTGCAGAGCGAGCGGCTGCTGCGCTTC 794
Qy 221 SerPheValTyrIleLeuThrGlyLeuThrValIleGlyAlaPheLeuAsnLeuVal 240
Db 795 AGCTTCGTCTACATCTTACGGCGCTCAGGCTCATCGCGCGCTTCTCAACCTCGTGGTG 854
Qy 241 LeuArgPheMetThrMetAsnAlaGluAspGluLysArgAspAlaGluHisArgAlaLeu 260
Db 855 CTGCGCTTCTATGACCATGACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 914
Qy 261 LeuThrHisAsnGlyGlnAlaValGlyLeuGlyLeuSerCysLeuSerGlySerLeu 280
Db 915 CTCAGCGCAACGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 953
Qy 281 GlyAspValArgProArgAspProValThrCysAlaAlaAlaAlaGlyValGlyVal 300
Db 954 GCGAGCGCGCACACTACGCGCACCGCGCTTCTCCAGCGCGCGCGCGCGCGCG 998
Qy 301 GlyValGlyGlySerGlyPheArgAsnValTyrAlaGluValLeuHisPheGlnSerMet 320
Db 999 -----GCGCGGCGCGCTTCGCGACGCTACGCGGAGGCTGCTGCACTTCCAGTCCATG 1052
Qy 321 CysSerCysLeuTyrTyrLysSerArgGluLysLeuGlnTyrSerIleProMetIleIle 340
Db 1053 TGCTCGTCTGCTGTGTACAGAGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1112
Qy 341 ProArgAspLeuSerThrSerAspThrCysValGluHisSerHisSerSerProGlyGly 360
Db 1113 CCGCGGAGCTTCTCCACGTCGACACGCTGCGTGGAGGAGGAGGAGGAGGAGGAGG 1172
Qy 361 GlyLysArgTyrSerAspThrProSerHisProCysLeuCysSerGlyThrGluArgSer 380
Db 1173 GCGGCGCGCTACAGGACGCGCGCTTCGCGAGCGCTGCTGCGGCGGCGCGCGCGCG 1232
Qy 381 AlaIleSerSerValSerThrGlyLeuHisSerLeuAlaAlaPheArgGlyLeuMetLys 400
Db 1233 GCCATCAGCTCGGTGTCCACGGGTCTGCAGAGCGCTGCTCCACCTTCGCGGCGCTCATGAG 1292
Qy 401 ArgArgSerSerVal 405
Db 1293 CGCAGGAGCTCGTG 1307

RESULT 11
AF065163
LOCUS Homo sapiens Kcnk3 channel mRNA linear PRI 29-MAY-2002
DEFINITION Homo sapiens Kcnk3 channel mRNA, complete cds.
ACCESSION AF065163
VERSION AF065163.1 GI:11093519
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2590)
Lopes, C.M., Gallagher, P.G., Buck, M.E., Butler, M.H. and
Goldstein, S.A.
Proton block and voltage gating are potassium-dependent in the
cardiac leak channel kcnk3
J. Biol. Chem. 275 (22), 16969-16978 (2000)
20287574
10748056
2 (bases 1 to 2590)
Goldstein, S.A.N.
Direct Submission
Submitted (13-MAY-1998) Section of Developmental Biology and
Biophysics, Department of Pediatrics, Yale University School of
Medicine, 295 Congress Avenue, New Haven, CT 06536, USA
Location/Qualifiers
1. 2590
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="heart"
126..1310
/note="two P domain potassium channel; cardiac potassium
channel; KCNK3; OAT1; TASK1; TBK1"
/codon_start=1
/product="Kcnk3 channel"
/protein_id="AAG29340.1"
/db_xref="GI:11093520"
/translation="MKQNVRLALIVCTFTLLVGAADFDALESEPELIERQRLER
QQLRARNYSQGGYELEKRVLRKPKAGVQWRFGSFFALTIVITIGYHAAPS
TDGKVPFCYFALLGIPLLTFMFQSLGERINTLVRLHRAKGLGMRADVSNMNV
LIQFSCISTLCGAAPAFSHYEHWTFFQAYYCFITLTTCFGDYALQKQALQTOP
QYVAFSPVYILTGLTVTIGAFNLVLRMTMAEDKRDHRAALLRNQOAGCGGG
GSAHTTDTASSTAAGGGRNVYAEVLHFQSMCSCLYKSRKLYSIPWILPRDLS
TSDTCVEQSHSPGGGRYSDTPRRCLCSGAPSAISSVSTGLHSLSTFRGLMKRRS
SV"
ORIGIN
Alignment Scores:
Pred. No.: 2,09e-148 Length: 2590
Score: 1819.00 Matches: 357
Percent Similarity: 90.37% Conservative: 9
Best Local Similarity: 88.15% Mismatches: 25
Query Match: 86.41% Indels: 14
DB: Gaps: 2
US-09-939-483-5 (1-405) x AF065163 (1-2590)
Qy 1 GluAsnValArgThrLeuAlaLeuIleValCysThrPheThrTyrLeuLeuValGlyAla 20
Db 135 CAGAACGTGCGCAGCTGGCGCTCATCTGTGCACTTACCTACCTGCTGGTGGCGCC 194
Qy 21 AlaValPheAspAlaLeuGluSerGluProGluMetIleGluArgGlnArgLeuGluLeu 40
Db 195 GCGGTCTTCGACGCGCTGGAGTCGAGCCGCGAGCTGATCGAGCGCGAGCTGAGCTG 254
Qy 41 ArgGlnLeuGluLeuArgAlaArgTyrAsnLeuSerGluGlyGlyTyrGluLeuGlu 60
Db 255 CGGACGAGGAGCTGCGGCGCGCTACAACTCAGCAGGCGGCTACGAGGAGCTGGAG 314
Qy 61 ArgValValLeuArgLeuLysProHisLysAlaGlyValGlnTyrArgPheAlaGlySer 80
Db 315 CGCGTCTGCTGCGCTCAAGCGCGCACAGCGCGCTGAGTGGCGCTTCGCGCGCTCC 374
Qy 81 PheTyrPheAlaIleThrValIleThrThrIleGlyTyrGlyHisAlaAlaProSerThr 100
Db 375 TTCTACTTCCGCATCACCCTCATCACCACCATCGGCTACGGGACGCGGACCGCACG 434
Qy 101 AspGlyGlyLysValPheCysMetPheTyrAlaLeuLeuGlyIleProLeuThrLeuIle 120
Db 435 GATGCGGCAAGGTTCTTCATGTTCTACGCGCTGCTGGGCATCCCGCTCACGCTCGTC 494


```

Db      1090  GCTGCGCCCTGGGCTGAGCTGCTGAGCGGTAGCTGCGGCGAGCGGCTGCGTCCC 1149
Qy      286  ArgSepProValThrCysAlaAlaAlaAlaGlyValGlyValGlyValGlyValGlySer 305
Db      1150  CGCAGCCAGTCAATGCGCTGCGGCGCGGAGCGCGTGGCGTGGCGTGGCGAGC 1209
Qy      306  GlyPheArgAenValTyAlaGluValLeuHisPheGlnSerMetCysSerCysLeuTyr 325
Db      1210  GGCTTCGCGACGCTATGCGGAGGTGTCACATCCAGTCCATGCTGCTGGTCTGG 1269
Qy      326  TyrIysSerArgGluLysLeuGlnTyrSerIleProMetIlelleProArgAspLeuSer 345
Db      1270  TACAGAGCCGCGAGAGCTGCTGCTGCTGATCCATCCCATGATCATCCGCGGAGCTCTCC 1329
Qy      346  ThrSerSepThrCysValGluHisSerHisSerSerProGlyGlyGlyGlyArgTyrSer 365
Db      1330  ACGTCCGACACCTGCGTGGAGCAGCAGCACATCTGTCGCGGAGCGCGCGCGCTACAGC 1389
Qy      366  AspThrProSerHisProCysLeuCysSerGlyThrGlnArgSerAlaIleSerSerVal 385
Db      1390  GACAGCCCTCACACCCCTGCTGTGCGAGCGGAGCAGCGCTCGGCGATCAGCTCGGTG 1449
Qy      386  SerThrGlyLeuHisSerLeuAlaAlaPheArgGlyLeuMetLysArgArgSerSerVal 405
Db      1450  TCCAGCGGCTGCGACAGCTGCGCTGCTGCGCGGCTCATGAAGCGCAGGAGCTCGGTG 1509

RESULT 14
AC102222/c
LOCUS   AC102222 143074 bp DNA linear HTG 21-OCT-2002
DEFINITION Mus musculus clone RP24-238P7, WORKING DRAFT SEQUENCE, 4 unordered pieces.
ACCESSION AC102222
VERSION   AC102222.3 GI:24182349
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 143074)
Birren,B., Nusbaum,C. and Lander,E.
Mus musculus, clone RP24-238P7
Unpublished
2 (bases 1 to 143074)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepei,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
Jones,C., Kamat,A., Karatas,A., Kellis,C., LaRocque,K.,
Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
McCarthy,M., McSwan,P., McKernan,K., McPheeters,R., Meldrim,J.,
Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Rettar,C., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 143074)
Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhgalter,B.,
Camarata,J., Chang,J., Chazaro,B., Choepei,Y., Collymore,A.,
Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,

```

```

Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hafez,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kellis,C., Landers,T., Levine,R.,
Lindblad-Toh,K., Liu,G., Maclean,C., Macdonald,P., Major,J.,
Matthews,C., McCarthy,M., Meldrim,J., Meneus,L., Mihova,T.,
Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,
Peterson,K., Phunkhang,P., Pierre,N., Raymond,C., Rettar,C.,
Rise,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schupback,R.,
Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Talamas,J., Tesfaye,S., Theodore,J., Topham,K.,
Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (21-OCT-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Oct 21, 2002 this sequence version replaced gi:22381186.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: L18232
Center clone name: 238_P7
----- Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 142160 bases at least Q40
Consensus quality: 142401 bases at least Q30
Consensus quality: 142477 bases at least Q20
Insert size: 134000; agarose-fp
Insert size: 142774; sum-of-contigs
Quality coverage: 11.8 in Q20 bases; agarose-fp
Quality coverage: 11.1 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 13454: contig of 13454 bp in length
* 13455 13554: gap of 100 bp
* 13555 16197: contig of 2643 bp in length
* 16198 16297: gap of 100 bp
* 16298 52990: contig of 36693 bp in length
* 52991 53090: gap of 100 bp
* 53091 143074: contig of 89984 bp in length.
FEATURES             Location/Qualifiers
     source            1..143074
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
                     /clone_lib="RP24-238P7"
     misc_feature      1..13454
                     /note="assembly_fragment"
                     /clone_end:SP6
                     /vector_side:left
     misc_feature      13555..16197
                     /note="assembly_fragment"
     misc_feature      16298..52990
                     /note="assembly_fragment"
     misc_feature      53091..143074
                     /note="assembly_fragment"

```

```
clone_end:17
vector_side:right"

ORIGIN
Alignment Scores:
Pred. No.: 7,35e-131 Length: 143074
Score: 1642.50 Matches: 224
Percent Similarity: 91.3% Conservative: 5
Best Local Similarity: 90.0% Mismatches: 16
Query Match: 78.03% Indels: 15
DB: 2 Gaps: 4

US-09-939-483-5 (1-405) x AC102222 (1-143074)

Qy 50 AenLeuSerGluGly-----GlyTyrGluGluLeuGluAArgValValLeuArgLeu 66
Db 121495 AACCTGCAAGTGGGAGGAGGAGGATGGGCAGAG---GAGGAGGGACCCCTGCCAGAC 121439

Qy 67 LysProHisLysAlaGlyValGlnTrpArgPheAlaGlySerPheTyrPheAlaIleThr 86
Db 121438 CAGCCCCAC-----AGCCTGTGCTTTCTCTCTCTCT 121409

Qy 87 ValIleThrThrIleGlyTyrGlyHisAlaAlaProSerThrAspGlyGlyLysValPhe 106
Db 121408 CCCCAGATCTTACAGGCTATGGTCAATGCGGCGCCACAGCAGGAGGCAAGGTGTTC 121349

Qy 107 CysMetPheTyrAlaLeuLeuGlyIleProLeuThrLeuIleMetPheGlnSerLeuGly 126
Db 121348 TGCATGTTCTACGGCTGCTGGGCATCCGCTCACACTAGTTCATGTTCCAGAGCTGGGT 121289

Qy 127 GluArgIleAenThrPheValArgTyrLeuLeuHisArgAlaLysArgGlyLeuGlyMet 146
Db 121288 GAACGCATCAACACCTTCGTGAGGTACCTGCTGCACCGCTGCCAAGAGGGGCTGGGCATG 121229

Qy 147 ArgHisAlaGluValSerMetAlaAenMetValLeuIleGlyPheValSerCysIleSer 166
Db 121228 CGGCACGCGGAGGTGCTCCATGCCCAACATGGTCTCATCGTTTCGTGTCATCATCAGC 121169

Qy 167 ThrLeuCysIleGlyAlaAlaAlaPheSerTyrTyrGluArgTyrPhePheGlnAla 186
Db 121168 ACGCTGTGCATCGCGGAGCTGCCTTCTCTTACTACGAGCGCTGACATTTCTTCCAGGCC 121109

Qy 187 TyrTyrTyrCysPheIleThrLeuThrThrIleGlyPheGlyAspTyrValAlaLeuGln 206
Db 121108 TATTACTACTGCTTATCACCCTCACCAACCATCGCTTTCGCGCATATGTGGCGCTGCAG 121049

Qy 207 LysAspGlnAlaLeuGlnThrGlnProGlnTyrValAlaPheSerPheValTyrIleLeu 226
Db 121048 AAGGACACGCGCTGCAGACGCGCGCAGTATGTGGCTTCAGCTTCGTGTATCATCTC 120989

Qy 227 ThrGlyLeuThrValIleGlyAlaPheLeuAenLeuValValLeuArgPheMetThrMet 246
Db 120988 ACGGSCCTCACGGTCACTCGCGCTTCTCTAACCTCGTGGTGTGCGATTTCATGACCATG 120929

Qy 247 AenAlaGluAseGluLysArgAspAlaGluHisArgAlaLeuLeuThrHisAenGlyCln 266
Db 120928 AACGCGGAGGACGAAAGCGTATGCGGAGCACCGCGCTGCTCACACACAGCGGCAG 120869

Qy 267 AlaValGlyLeuGlyLysSerCysLeuSerGlySerLeuGlyAsePheValArgPro 285
Db 120868 GCTGTGCGCTTGGTGGCTGAGTGTGCTGAGCGGTAGCTGCGGCGCGGCGGTGCGTCC 120809

Qy 286 ArgAspProValThrCysAlaAlaAlaAlaGlyValGlyValGlyValGlySer 305
Db 120808 CGCGACCCAGTCACATGCTGCGCGCGGAGCGGTGGCGTGGGCGTGGTGGCAGC 120749

Qy 306 GlyPheArgAenValTyrAlaGluValLeuHisPheGlnSerMetCysSerCysIleuTrp 325
Db 120748 GGCCTCCGCAAGCTATGCGGAGGTGCTGCACATTCACATGCTCATGCTGCTGCTG 120689

Qy 326 TyrLysSerArgGluLysLeuGlnTyrSerIleProMetIleIleProArgAspLeuSer 345
Db 120688 TACAAGACCGCGGAGAGCTGCAGTACTCCATCCCATGATCATCCCGCGGACCTCTCC 120629

Qy 346 ThrSerAspThrCysValGluHisSerHisSerSerProGlyGlyGlyArgTyrSer 365
Db 120628 ACGTCCGACACCTGCGTGGAGCACAGCACTCGTCCGCGGAGCGCGCGCTACAGC 120569

Qy 366 AspThrProSerHisProCysLeuCysSerGlyThrGlnArgSerAlaIleSerVal 385
Db 120568 GACACGCGCTCACACCCCTGCTGTGAGCGGGAGCAGCGGCTCGGCATCAGTCCGTG 120509

Qy 386 SerThrGlyLeuHisSerLeuAlaAlaPheArgGlyLeuMetLysArgSerVal 405
Db 120508 TCCAGGCGCTGCACAGCTGGCTTCCTCCGCGCTCATGAAGCGCAGAGCTCGGTG 120449

RESULT 15
AC105298 258789 bp DNA linear ROD 16-NOV-2002
LOCUS Mus musculus chromosome 5 clone rp23-224j9 strain C57BL/6J,
DEFINITION complete sequence.
AC105298
VERSION AC105298.21 GI:25046377
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Zhou,L., Fu,Y., Shi,R., Wu,J. and Roe,B.A.
TITLE 1 (bases 1 to 258789)
JOURNAL Mus musculus BAC Clone rp23-224j9
REFERENCE
AUTHORS Zhou,L., Fu,Y., Shi,R., Wu,J. and Roe,B.A.
TITLE 2 (bases 1 to 258789)
JOURNAL Direct Submission
AUTHORS Zhou,L., Fu,Y., Shi,R., Wu,J. and Roe,B.A.
TITLE Submitted (29-DEC-2001) Department Of Chemistry And Biochemistry,
JOURNAL The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
REFERENCE
AUTHORS Zhou,L., Fu,Y., Shi,R., Wu,J. and Roe,B.A.
TITLE 3 (bases 1 to 258789)
JOURNAL Direct Submission
AUTHORS Zhou,L., Fu,Y., Shi,R., Wu,J. and Roe,B.A.
TITLE Submitted (27-AUG-2002) Department Of Chemistry And Biochemistry,
JOURNAL The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
REFERENCE
AUTHORS Zhou,L., Fu,Y., Shi,R., Wu,J. and Roe,B.A.
TITLE 4 (bases 1 to 258789)
JOURNAL Direct Submission
AUTHORS Zhou,L., Fu,Y., Shi,R., Wu,J. and Roe,B.A.
TITLE Submitted (01-SEP-2002) Department Of Chemistry And Biochemistry,
JOURNAL The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
REFERENCE
AUTHORS Zhou,L., Fu,Y., Shi,R., Wu,J. and Roe,B.A.
TITLE 5 (bases 1 to 258789)
JOURNAL Direct Submission
AUTHORS Zhou,L., Fu,Y., Shi,R., Wu,J. and Roe,B.A.
TITLE Submitted (16-NOV-2002) Department Of Chemistry And Biochemistry,
JOURNAL The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
COMMENT On Nov 16, 2002 this sequence version replaced gi:22597523.
----- Genome Center
Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
Center code:UOKNOR
-----
FEATURES
source Location/Qualifiers
1. 258789
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/chromosome="5"
/clone="rp23-224j9"
/clone_lib="RPCI - 23 Female (C57BL/6J) Mouse BAC Library"

ORIGIN
Alignment Scores:
Pred. No.: 1.54e-130 Length: 258789
Score: 1642.50 Matches: 324
```

Percent Similarity:	91.3%	Conservative:	5
Best Local Similarity:	90.0%	Mismatches:	16
Query Match:	78.0%	Indels:	15
DB:	10	Gaps:	4

US-09-939-483-5 (1-405) x AC105298 (1-258789)

Qy	50	AsnLeuSerGluGly-----GlyTyrGluGluLeuGluArgValValleuArgLeu	66
Db	111272	AACCTGCAAGTGGGGAGGGAGGGGATGGGCAGAG---GAGGAGGGACCCCTCGGCAGAC	111216
Qy	67	LysProHisLysAlaGlyValGlnTrpArgPheAlaGlySerPheTyrPheAlaIleThr	86
Db	111215	CAGCCCCAC-----AGCGTGTGCTTCTCTCTCTCT	111186
Qy	87	ValIleThrThrIleGlyTyrGlyHisAlaProSerThrAspGlyGlyLysValPhe	106
Db	111185	CCCGGATCTCTACAGGCTATGTGTCGGCGCCAGCAGCAGCAGGAGCGAAGGTGTTCT	111126
Qy	107	CysMetPheTyrAlaLeuLeuGlyIleProLeuThrLeuIleMetPheGlnSerLeuGly	126
Db	111125	TGCATGTTCTACGCGCTGCTGGGCATCCCGTCACTAGTCAATGTTCCAGAGCCTGGGT	111066
Qy	127	GluArgIleAsnThrPheValArgTyrLeuLeuHisArgAlaLysArgGlyLeuGlyMet	146
Db	111065	GAACGCATCAACACCTTCGTAGGTACCTGTCTGCACCGTGCACAGAGGGGGCTGGGCATG	111006
Qy	147	ArgHisAlaGluValSerMetAlaAsnMetValLeuIleGlyPheValSerCysIleSer	166
Db	111005	CGGCACGCGAGGTGTCATGGCCAACTGFGTCTCATCGGTTTCGTGTCGATCAGC	110946
Qy	167	ThrLeuCysIleGlyValAlaAlaPheSerTyrTyrGluArgTyrThrPhePheGlnAla	186
Db	110945	ACGCTGTGCATCGCGCAGCTGCCTTCTCTACTACGAGCGCTGGACTTCTTCAGGCGC	110886
Qy	187	TyrTyrTyrCysPheIleThrLeuThrThrIleGlyPheGlyAspTyrValAlaLeuGln	206
Db	110885	TATTACTACTGTTTCATCACCTCCACCACCTCGCTTCGGCGCATATGTGGCGTGCAG	110826
Qy	207	LysAspGlnAlaLeuGlnThrGlnProGlnTyrValAlaPheSerPheValTyrIleLeu	226
Db	110825	AAGNACGAGCGCTGCAGACGCGCGCATGTGTGGCCCTCAGCTTCTGTGTACATCCTC	110766
Qy	227	ThrGlyLeuThrValIleGlyAlaPheLeuAsnLeuValValLeuArgPheMetThrMet	246
Db	110765	ACGGCGCTCACGTCATCGCGCCCTCTCTCAACCTCGTGTGTCGATTCATGACCATG	110706
Qy	247	AsnAlaGluAspGluLysArgAspAlaGluHisArgAlaLeuLeuThrHisGlnGlyGln	266
Db	110705	AACGCCGAGGACGAGAAGCGTATCGGAGCACCGCGCCCTGCTCAGGCACAAACGGCCAG	110646
Qy	267	AlaValGlyLeuGlyGlyLeuSerCysLeuSerGlySerLeuGlyAsp---ValArgPro	285
Db	110645	GCTGTGCGCCTGGGTGGCTTCAGCTGCCGTAGCGGTAGCTGGCGCAGCGGCTGCTCCC	110586
Qy	286	ArgAspProValThrCysAlaAlaAlaGlyGlyValGlyValGlyValGlyGlySer	305
Db	110585	CGCGACCCAGTACATATGCGTCCGCGCGGAGCGTGGCGCGTGGCGCGTGGTGGCAGC	110526
Qy	306	GlyPheArgAsnValTyrAlaGluValLeuHisPheGlnSerMetCysSerCysLeuTrp	325
Db	110525	GGCTTCCGCAACGTTATGCGGAGTGTGTGACATTCCTCCAGTCCATGTGCTGCTGCTGG	110466
Qy	326	TyrIysSerArgGluLysLeuGlnTyrSerIleProMetIleIleProArgAspLeuSer	345
Db	110465	TACAAGAGCCGCGAAGCTGACGTACTCCATCCCGCATGATCATCCCGGGACCTCTCC	110406
Qy	346	ThrSerAspThrCysValClnHisSerHisSerSerProGlyGlyGlyArgTyrSer	365
Db	110405	ACGTCGACACTCGTGTGGAGCACAGCACTCGTCGCGGAGGCGCGCGCTACAGC	110346
Qy	366	AspThrProSerHisProCysLeuCysSerGlyThrGlnArgSerAlaIleSerVal	385

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2005, 22:44:19 ; Search time 170 Seconds
(without alignments)
1219.953 Million cell updates/sec

Title: US-09-939-483-5
Perfect score: 2105
Sequence: 1 ENVRTALIVCTFTYLLVGA.....STGLHSLAAPRLMKRRSSV 405

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2090.5	99.3	409	1	CIW3_MOUSE
2	2065.5	98.1	411	1	CIW3_RAT
3	1944	92.4	392	2	Q9ESM5
4	1819	86.4	394	1	CIW3_HUMAN
5	1519.5	72.2	301	2	Q9ESM4
6	1507.5	71.6	299	2	Q9QX34
7	1123	53.3	374	2	Q63Z10
8	1100	52.3	374	1	CIW9_HUMAN
9	1062.5	50.5	365	1	CIW9_CAVPO
10	994	47.2	396	2	Q923V6
11	955.5	45.4	395	2	Q9JLD4
12	909	43.2	237	1	CIW9_RAT
13	886.5	42.1	318	1	CIWF_RAT
14	836.5	39.7	330	1	CIWF_HUMAN
15	800	38.0	329	2	O17185
16	757.5	36.0	345	2	Q7QC61
17	753	35.8	340	2	Q9VHE0
18	748	35.5	307	2	Q7PZH9
19	732.5	34.8	270	2	Q9JL57
20	726.5	34.5	398	2	Q9VFS9
21	611	29.0	364	2	O76790
22	501	23.8	121	2	Q867A3
23	369	17.5	405	1	CIWD_MOUSE
24	364.5	17.3	405	1	CIWD_RAT
25	361.5	17.2	408	1	CIWD_HUMAN
26	360.5	17.1	331	2	Q8AV15
27	355	16.9	309	1	CIWG_HUMAN
28	352.5	16.7	453	2	Q8BZB0
29	352.5	16.7	535	2	Q8BUW1
30	352.5	16.7	538	1	CIWA_HUMAN
31	352.5	16.7	538	1	CIWA_RAT

32	352.5	16.7	538	2	Q6Q834
33	352.5	16.7	543	2	Q6B014
34	348	16.5	294	2	Q6X6Z5
35	345	16.4	411	1	CIW2_MOUSE
36	342	16.2	426	2	Q920B6
37	341	16.2	323	2	Q6PSI1
38	341	16.2	393	1	CIW4_HUMAN
39	341	16.2	414	2	Q6P6P9
40	340.5	16.2	262	2	Q6X6Z3
41	338	16.1	411	2	Q8HY88
42	338	16.1	426	1	CIW2_HUMAN
43	337	16.0	411	2	Q9NET2
44	334.5	15.9	336	1	CIW1_HUMAN
45	334.5	15.9	336	2	Q9Z2T2

ALIGNMENTS

RESULT 1
CIW3_MOUSE
ID CIW3_MOUSE STANDARD; PRT; 409 AA.
AC Q351L1: Q35163;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium channel subfamily K member 3 (Acid-sensitive potassium
DE channel protein TASK-1) (TWIK-related acid-sensitive K+ channel 1)
DE (Cardiac two-pore background K+ channel) (CTBAK-1) (Two pore potassium
DE channel KT3.1).
GN Names=Kcnk3; Synonyms=Ctbak, TASK, Task1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=98165556; PubMed=9506712;
RA Kim D., Fujita A., Horio Y., Kurachi Y.;
RT "Cloning and functional expression of a novel cardiac two-pore
RT background K+ channel (CTBAK-1).";
RL Circ. Res. 82:513-518 (1998).
RN [2]
RC TISSUE=Heart;
RX MEDLINE=20287574; PubMed=10748056; DOI=10.1074/jbc.M001948200;
RA Lopes C.M., Gallagher P.G., Buck M.E., Butler M.H., Goldstein S.A.;
RT "Proton block and voltage gating are potassium-dependent in the
RT cardiac leak channel Kcnk3.";
RL J. Biol. Chem. 275:16969-16978 (2000).
RN [3]
RP SEQUENCE OF 4-409 FROM N.A.
RX MEDLINE=97459932; PubMed=9312005; DOI=10.1093/emboj/16.17.5464;
RA Duprat F., Lesage F., Fink M., Reyes R., Heurteaux C., Lazdunski M.;
RT "TASK, a human background K+ channel to sense external pH variations
RT near physiological pH.";
RL EMBO J. 16:5464-5471 (1997).
CC -I- FUNCTION: pH-dependent, voltage-insensitive, background potassium
CC channel protein. Rectification direction results from potassium
CC ion concentration on either side of the membrane. Acts as an
CC outward rectifier when external potassium concentration is low.
CC When external potassium concentration is high, current is inward
CC (by similarity).
CC -I- SUBUNIT: Homodimer (Potential).
CC -I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -I- TISSUE SPECIFICITY: Very strong expression in heart, also detected
CC in kidney, brain, skin, testis, lung, skeletal muscle, small
CC intestine and stomach. Not detected in liver, thymus or spleen.
CC -I- MISCELLANEOUS: Inactivated by barium.
CC -I- SIMILARITY: Belongs to the two pore domain potassium channel
CC (TC 1.A.1.8) family.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announcement/> or send an email to license@isb-sib.ch).

EMBL; AB008537; BAA25436.1; -
 EMBL; AP241798; AAF81418.1; -
 EMBL; AP242508; AAF81418.1; JOINED.
 EMBL; AF065162; AAG29339.1; -
 EMBL; AF006824; AAC53367.1; -
 EMBL; AB013345; BAA28349.1; -
 MGD; MGI:1100509; Kcnk3.
 InterPro; IPR005821; Ion trans.
 InterPro; IPR003280; K+channel_2pore.
 InterPro; IPR001622; K+channel_pore.
 InterPro; IPR005406; TASK1_channel.
 InterPro; IPR003092; TASK1_channel.
 Pfam; PF00520; Ion trans.1.
 PRINTS; PR01333; 2PORECHANNEL.
 PRINTS; PR01584; TASK1CHANNEL.
 PRINTS; PR01095; TASKCHANNEL.
 Glycoprotein; Ion transport; Ionic channel; Potassium;
 Potassium channel; Transmembrane; Transport; Voltage-gated channel.
 DOMAIN 1 8 Cytoplasmic (Potential).
 TRANSMEM 9 29 Potential.
 DOMAIN 78 101 Pore-forming 1 (Potential).
 TRANSMEM 108 128 Potential.
 DOMAIN 129 158 Cytoplasmic (Potential).
 TRANSMEM 159 179 Potential.
 DOMAIN 184 207 Pore-forming 2 (Potential).
 TRANSMEM 223 243 Potential.
 DOMAIN 244 409 Cytoplasmic (Potential).
 CARBOHYD 53 53 N-linked (GlcNAc...) (Potential).
 CONFLICT 4 4 Q -> E (in Ref. 3).
 CONFLICT 123 123 V -> I (in Ref. 3).
 SEQUENCE 409 AA; 45068 MW; 352336E011AAC5687 CRC64;

Query Match 99.3%; Score 2090.5; DB 1; Length 409;
 Best Local Similarity 99.3%; Pred. No. 1.le-153;
 Matches 403; Conservative 2; Mismatches 0; Indels 1; Gaps 1;
 QY 1 ENVRTALIVCTFTLLVGAADFDALESEPEMERORLELRARVNLSEGGVEELE 60
 Db 4 QNVRTALIVCTFTLLVGAADFDALESEPEMERORLELRARVNLSEGGVEELE 63
 QY 61 RVVLRKPKHAGVQWRFAGSFYFAITVITIGVGHAAAPSTDGKVFCEFYALLGIPLTLI 120
 Db 64 RVVLRKPKHAGVQWRFAGSFYFAITVITIGVGHAAAPSTDGKVFCEFYALLGIPLTLV 123
 QY 121 MFQSLGERINTFVRYLLHRAKGLGNHAEVSMANVLI GFVSCISTLCIGAAAFSYR 180
 Db 124 MFQSLGERINTFVRYLLHRAKGLGNHAEVSMANVLI GFVSCISTLCIGAAAFSYR 183
 QY 181 WTFQFYVYCFITLTITIGFDVVALQDALOTPOYVAFSFVYILTGLTVIGAFINLVV 240
 Db 184 WTFQFYVYCFITLTITIGFDVVALQDALOTPOYVAFSFVYILTGLTVIGAFINLVV 243
 QY 241 LRFMTNNAEDKRAEHRALLTHNGQAVGLGSLCSLSGLSD-VRPDPVTCAAAAGGVG 299
 Db 244 LRFMTNNAEDKRAEHRALLTHNGQAVGLGSLCSLSGLSDGVPRDPVTCAAAAGGVG 303
 QY 300 VVGSGGFNVVAEVLHFSQMSCLWYKREKLQVSIPIIIPRDLSTSTCVHEHSHSPG 359
 Db 304 VVGSGGFNVVAEVLHFSQMSCLWYKREKLQVSIPIIIPRDLSTSTCVHEHSHSPG 363
 QY 360 GGGRYSDTFPSHPCSCGTQRSATSSVSTGLHSLAAPRGLMKRRSSV 405
 Db 364 GGGRYSDTFPSHPCSCGTQRSATSSVSTGLHSLAAPRGLMKRRSSV 409

RESULT 2
 CIW3_RAT STANDARD; PRT; 411 AA.
 ID OS4912;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Potassium channel subfamily K member 3 (Acid-sensitive potassium channel protein TASK-1) (TWIK-related acid-sensitive K+ channel 1)
 DE (two pore potassium channel KT3.1).
 DE Name=Kcnk3; Synonyms=Task, Task1;
 GN Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cerebellum;
 RX MEDLINE=98099797; PubMed=9437008;
 RA Leonoudakis D., Gray A.T., Winegar B.D., Kindler C.H., Harada M.,
 RA Taylor D.M., Chavez R.A., Forsayeth J.R., Yost C.S.;
 RT "An open rectifier potassium channel with two pore domains in tandem cloned from rat cerebellum";
 RL J. Neurosci. 18:868-877(1998).
 CC -!- FUNCTION: pH-dependent, voltage-insensitive, background potassium channel protein. Rectification direction results from potassium ion concentration on either side of the membrane. Acts as an outward rectifier when external potassium concentration is low. When external potassium concentration is high, current is inward (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- TISSUE SPECIFICITY: Strongest expression in heart. Moderate expression in lung and brain. Low levels in liver, kidney and skeletal muscle.
 CC -!- MISCELLANEOUS: Inhibited by extracellular acidification, zinc, bupivacaine and phenytoin. Activated by protein kinase A.
 CC -!- SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announcement/> or send an email to license@isb-sib.ch).

Query Match 98.1%; Score 2065.5; DB 1; Length 411;

Best Local Similarity 98.08; Pred. No. 9.4e-152;
Matches 400; Conservative 3; Mismatches 2; Indels 3; Gaps 2;

```

QY 1 ENVRTLALIVCTFTYLLVGAADFDALESEPEMTERQRLQLELRARVNLSEGGYEEL 60
   :|||||
DB 4 QNVRTLALIVCTFTYL-----LES-----ELRQLELRARVNLSEGGYEEL 44

QY 61 RVVRLKPKHAGVQWRPAGSFYFAITVITTYGHAAPSTDDGGKVCFCMFVALLGIPITLI 120
   :|||||
DB 64 RVVRLKPKHAGVQWRPAGSFYFAITVITTYGHAAPSTDDGGKVCFCMFVALLGIPITLV 123

QY 121 MFQSLGERINTFVRYLLHRAKRGGLMRHAEVSMANVMVLIGFVSCISFLCIGAAAFSYER 180
   :|||||
DB 124 MFQSLGERINTFVRYLLHRAKRGGLMRHAEVSMANVMVLIGFVSCISFLCIGAAAFSYER 183

QY 181 WTFPQAYYYCFITLTTIGFGDYVALQDQALQTPQYVAFSFYVILTGLTVIGAFNLVV 240
   :|||||
DB 184 WTFPQAYYYCFITLTTIGFGDYVALQDQALQTPQYVAFSFYVILTGLTVIGAFNLVV 243

QY 241 LRFMTWNAEDKDAEHRALLTHNGQAVGLGGLSCLSGSLGD--VRPRDPVTCAAAAG--G 297
   :|||||
DB 244 LRFMTWNAEDKDAEHRALLTHNGQAVGLGGLSCLSGSLGDGVRPRDPVTCAAAAGGMG 303

QY 298 VGVGVGSGFRNVYAELVHFQSMCSCLYKRSREKLOYSIPMIIPRDLSTSDTCTVEHSHS 357
   :|||||
DB 304 VGVGVGSGFRNVYAELVHFQSMCSCLYKRSREKLOYSIPMIIPRDLSTSDTCTVEHSHS 363

QY 358 PGGGGRYSDTPSHPCLCSTGQTSRQSAISSVSTGLHSLAARFGLMKRRSSV 405
   :|||||
DB 364 PGGGGRYSDTPSHPCLCSTGQTSRQSAISSVSTGLHSLATFRGLMKRRSSV 411

```

RESULT 3

```

Q9ESM5 PRELIMINARY; PRT; 392 AA.
AC Q9ESM5
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE TASK1 splice bvariant (TASK1b).
GN Name=KCNK3b;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Ohya S., Kiteukawa M., Imaizumi Y.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the two pore domain potassium channel
   (TC 1.A.1.8) family.
CC EMBL: AB048823; BAB16710.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0005216; F:ion channel activity; IEA.
DR GO: GO:0005267; F:potassium channel activity; IEA.
DR GO: GO:0006811; P:ion transport; IEA.
DR GO: GO:0006813; P:potassium ion transport; IEA.
DR InterPro: IPR005821; Ion trans.
DR InterPro: IPR003280; K+channel_2pore.
DR InterPro: IPR001622; K+channel_pore.
DR InterPro: IPR005406; TASK1_channel.
DR InterPro: IPR003092; TASK1_channel.
DR Pfam: PF00520; Ion trans. 1.
DR PRINTS: PR01333; 2FOREKCHANNEL.
DR PRINTS: PR01584; TASK1CHANNEL.
DR PRINTS: PR01095; TASKCHANNEL.
KW Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 392 AA; 43150 MW; F5438B12AAD7FB1B CRC64;

```

Query Match 92.48; Score 1944; DB 2; Length 392;
Best Local Similarity 93.44; Pred. No. 2.3e-142;
Matches 381; Conservative 3; Mismatches 2; Indels 22; Gaps 4;

```

QY 1 ENVRTLALIVCTFTYLLVGAADFDALESEPEMTERQRLQLELRARVNLSEGGYEEL 60
   :|||||
DB 4 QNVRTLALIVCTFTYL-----LES-----ELRQLELRARVNLSEGGYEEL 44

QY 61 RVVRLKPKHAGVQWRPAGSFYFAITVITTYGHAAPSTDDGGKVCFCMFVALLGIPITLI 120
   :|||||
DB 45 RVVRLKPKHAGVQWRPAGSFYFAITVITTYGHAAPSTDDGGKVCFCMFVALLGIPITLV 104

QY 121 MFQSLGERINTFVRYLLHRAKRGGLMRHAEVSMANVMVLIGFVSCISFLCIGAAAFSYER 180
   :|||||
DB 105 MFQSLGERINTFVRYLLHRAKRGGLMRHAEVSMANVMVLIGFVSCISFLCIGAAAFSYER 164

QY 181 WTFPQAYYYCFITLTTIGFGDYVALQDQALQTPQYVAFSFYVILTGLTVIGAFNLVV 240
   :|||||
DB 165 WTFPQAYYYCFITLTTIGFGDYVALQDQALQTPQYVAFSFYVILTGLTVIGAFNLVV 224

QY 241 LRFMTWNAEDKDAEHRALLTHNGQAVGLGGLSCLSGSLGD--VRPRDPVTCAAAAG--G 297
   :|||||
DB 225 LRFMTWNAEDKDAEHRALLTHNGQAVGLGGLSCLSGSLGDGVRPRDPVTCAAAAGGMG 284

QY 298 VGVGVGSGFRNVYAELVHFQSMCSCLYKRSREKLOYSIPMIIPRDLSTSDTCTVEHSHS 357
   :|||||
DB 285 VGVGVGSGFRNVYAELVHFQSMCSCLYKRSREKLOYSIPMIIPRDLSTSDTCTVEHSHS 344

QY 358 PGGGGRYSDTPSHPCLCSTGQTSRQSAISSVSTGLHSLAARFGLMKRRSSV 405
   :|||||
DB 345 PGGGGRYSDTPSHPCLCSTGQTSRQSAISSVSTGLHSLATFRGLMKRRSSV 392

RESULT 4
CIW3_HUMAN STANDARD; PRT; 394 AA.
AC Q14639;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium channel subfamily K member 3 (Acid-sensitive potassium
   channel protein TASK-1) (TWIK-related acid-sensitive K+ channel 1)
   (Two pore potassium channel KT3.1).
GN Name=KCNK3; Synonyms=TASK, TASK1;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=97459932; PubMed=9312005; DOI=10.1093/emboj/16.17.5464;
RA Duprat F., Lesage F., Fink M., Reyes R., Heurteaux C., Lazdunski M.;
RT "TASK, a human background K+ channel to sense external pH variations
   near physiological pH.";
RL EMBO J. 16:5464-5471(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Lopes C.M.B., Gallagher P.G., Buck M.E., Butler M.H.,
RA Goldstein S.A.N.;
RT "Proton block and voltage-gating are potassium-dependent in the
   cardiac leak channel Kcnk3.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP ACTIVATION.
RX MEDLINE=99254548; PubMed=10321245; DOI=10.1038/8084;
RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
RT "Inhalational anesthetics activate two-pore-domain background K+
   channels.";
RL Nat. Neurosci. 2:422-426(1999).
RN [4]
RP MUTAGENESIS OF HIS-98.
RX MEDLINE=21535313; PubMed=11680614;
RA Ashmore I., Goodwin P.A., Stanfield P.R.;
RT "TASK-5, a novel member of the tandem pore K+ channel family.";

```


RESULT 6	Q90X34	PRELIMINARY;	PRT;	299 AA.
ID	Q90X34	PRELIMINARY;	PRT;	299 AA.
AC	Q90X34			
DT	01-MAY-2000	(TrEMBLrel. 13, Created)		
DT	01-MAY-2000	(TrEMBLrel. 13, Last sequence update)		
DE	01-JUN-2003	(TrEMBLrel. 24, Last annotation update)		
DE	Putative potassium channel DP4 (Fragment).			
GN	Name=Kcnk3;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
OX	[1]			
RN	SEQUENCE FROM N.A.			
RP	Gan L., Joiner W.J., Quinn A.M., Wang L.-Y., Hughes T.,			
RA	Kaczmarek L.K.,			
RA	Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.			
RL	-!- SIMILARITY: Belongs to the two pore domain potassium channel			
CC	(TC 1.A.1.8) family.			
CC	EMBL; AF022821; AAD09338.1; -			
DR	MGD; MGI:1100509; Kcnk3			
DR	GO; GO:0005615; C:extracellular space; TAS.			
DR	GO; GO:0016021; C:integral to membrane; TAS.			
DR	InterPro; IPR005821; Ion trans.			
DR	InterPro; IPR003280; K+channel_2pore.			
DR	InterPro; IPR001622; K+channel_pore.			
DR	InterPro; IPR005406; TASK1_channel.			
DR	InterPro; IPR003092; TASK_channel.			
DR	Pfam; PF00520; Ion trans; 1.			
DR	PRINTS; PR01333; 2PORECHANNEL.			
DR	PRINTS; PR01584; TASK1CHANNEL.			
DR	PRINTS; PR01095; TASKCHANNEL.			
KW	Ion transport; Ionic channel; Transmembrane; Transport.			
FT	NON_TER 1			
FT	NON_TER 299			
FT	SEQUENCE 299 AA; 33325 MW; DCD41D8A212939C4 CRC64;			
QY	Query Match 71.6%; Score 1507.5; DB 2; Length 299;			
QY	Best Local Similarity 99.3%; Pred. No. 1.1e-108;			
QY	Matches 294; Conservative 1; Mismatches 0; Indels 1; Gaps 1;			
QY	1 ENVRTALIVCTFTYLLVGAADFALSEPEMTERQRLERQLELRARYNLSEGGVEELE 60			
QY				
QY	2 ENVRTALIVCTFTYLLVGAADFALSEPEMTERQRLERQLELRARYNLSEGGVEELE 61			
QY				
QY	61 RVVRLKPKHAGVQWRFGSFYFAITVTTIGYGHAAFPSTGGKVFQVCFYALLGIPLTLI 120			
QY				
QY	62 RVVRLKPKHAGVQWRFGSFYFAITVTTIGYGHAAFPSTGGKVFQVCFYALLGIPLTLV 121			
QY				
QY	121 MFQSLGERINTFVRYLLHRAKRGGLGMRHAESVMANNVLIQVSCISTLCIGAAAFSYYER 180			
QY				
QY	122 MFQSLGERINTFVRYLLHRAKRGGLGMRHAESVMANNVLIQVSCISTLCIGAAAFSYYER 181			
QY				
QY	181 WFFQAYYYCFITLTITIGFDYVALQKQALQTOQVYVAFSVVILTGLTVIGAFNLVV 240			
QY				
QY	182 WFFQAYYYCFITLTITIGFDYVALQKQALQTOQVYVAFSVVILTGLTVIGAFNLVV 241			
QY				
QY	241 LRPMTWNAEDEKRAEHRALLTHNGQAVGLGSLGSLGSD -VRPDPVTCAAA 295			
QY				
QY	242 LRPMTWNAEDEKRAEHRALLTHNGQAVGLGSLGSLGSD -VRPDPVTCAAA 297			
QY				
RESULT 7	Q63210	PRELIMINARY;	PRT;	374 AA.
ID	Q63210	PRELIMINARY;	PRT;	374 AA.
AC	Q63210			
DT	25-OCT-2004	(TrEMBLrel. 28, Created)		
DT	25-OCT-2004	(TrEMBLrel. 28, Last sequence update)		
DE	25-OCT-2004	(TrEMBLrel. 28, Last annotation update)		
DE	Hypothetical protein.			

Db 281 ----HGRQRYKAEVTDLQSVCSMCVRSHE---YTSRMVSHQNSPSSKLNPFVHSISYK 333
QY 357 ----SPGGGRYSDTSHCLCSGTORSALISSVSTGLHSLAARGLMKRRSV 405
Db 334 IBEISPS-----TLKNSLPSPSSVSPGLSHFTDKHRLMKRRKSI 374

RESULT 8
CIW9_HUMAN
ID CIW9_HUMAN STANDARD; PRT; 374 AA.
AC Q9NPC2;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium channel subfamily K member 9 (Acid-sensitive potassium
channel protein TASK-3) (TWIK-related acid-sensitive K+ channel 3)
DE (two pore potassium channel KT3.2).
GN Names=KCNK9; Synonyms=TASK3;
OS Homo sapiens (Human).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20287530; PubMed=10747866; DOI=10.1074/jbc.M000030200;
RA Rajan S., Wischmeyer E., Liu G.X., Preisig-Mueller R., Daut J.,
RA Karschin A., Dorst C.;
RA "TASK-3, a novel tandem pore domain acid-sensitive K+ channel. An
RT extracellular histidine as pH sensor";
RL J. Biol. Chem. 275:16650-16657(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Cerebellum;
RX PubMed=11042359; DOI=10.1016/S0169-328X(00)00183-2;
RA Chapman C.G., Meadows H.J., Godden R.J., Campbell D.A., Duckworth M.,
RA Kelsell R.E., Murdock P.R., Randall A.D., Rennie G.I., Gloger I.S.;
RT "Cloning, localisation and functional expression of a novel human,
RT cerebellum specific, two pore domain potassium channel";
RL Brain Res. Mol. Brain Res. 82:74-83(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Girard C., Lesage F., Tinel N., Lazdunski M.;
RT "Human Task-3, a novel 2P domain potassium channel related to Task.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=21324619; PubMed=11431495;
RA Vega-Saenz de Miera E., Lau D.H.P., Zhadina M., Pountney D.,
RA Coetzee W.A., Rudy B.;
RT "KT3.2 and KT3.3, two novel human two-pore K(+) channels closely
RT related to TASK-1";
RL J. Neurophysiol. 86:130-142(2001).
CC -!- FUNCTION: pH-dependent, voltage-insensitive, background potassium
CC channel protein.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: Mainly found in the cerebellum. Also found in
CC adrenal gland, kidney and lung.
CC -!- MISCELLANEOUS: Inhibited by phorbol 12-myristate 13-acetate (PMA).
CC Insensitive to changes in the pH range of 7-8.
CC -!- SIMILARITY: Belongs to the two pore domain potassium channel
CC (TC 1.A.1.8) family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
QR EMBL; AF212829; AAF63708.1; -;
DR EMBL; AF248241; AAG31730.1; -;
QR EMBL; AF279809; AAF85982.1; -;

DR BMBL; AF257080; AAG33126.1; -;
DR Genew; HGNC:6283; KCNK9.
DR MIM; 605874; -;
DR GO; GO:0005624; C:membrane fraction; NAS.
DR GO; GO:0005267; P:potassium channel activity; NAS.
DR GO; GO:0006813; P:potassium ion transport; NAS.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR003280; K+channel_2pore.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR005407; TASK3_channel.
DR InterPro; IPR003092; TASK3_channel.
DR Pfam; PF00520; Ion trans_1.
DR PRINTS; PR01333; 2POREKCHANNEL.
DR PRINTS; PR01585; TASK3CHANNEL.
DR PRINTS; PR01095; TASKCHANNEL.
KW Glycoprotein; Ion transport; Ionic channel; Potassium;
KW Potassium channel; Transmembrane; Voltage-gated channel.
FT DOMAIN 1 8
FT TRANSMEM 9 29 Cytoplasmic (Potential).
FT DOMAIN 78 101 Pore-forming 1 (Potential).
FT TRANSMEM 108 128 Potential.
FT DOMAIN 129 158 Cytoplasmic (Potential).
FT TRANSMEM 159 179 Potential.
FT DOMAIN 184 207 Pore-forming 2 (Potential).
FT TRANSMEM 219 239 Potential.
FT DOMAIN 240 374 Cytoplasmic (Potential).
FT CARBOHYD 53 53 N-linked (GlcNAc...), (Potential).
SQ SEQUENCE 374 AA; 42263 MW; 8A19AEF5A4D7F38 CRC64;
Query Match 52.3%; Score 1100; DB 1; Length 374;
Best Local Similarity 55.4%; Pred. No. 5.6e-77;
Matches 229; Conservative 48; Mismatches 86; Indels 50; Gaps 5;
QY 1 ENVRTALIVCTFTYLLVGAADVDALESEPEMIEQRLELRLELRARVNLSEGGYEEL 60
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 63
4 QNVRTLSLIVCTFTYLLVGAADVDALESDHEMREBEKKAEBIRIKGKYNISSEYRQLE
QY 61 RYVLRLEKHKAGVQWRFAGSFYFALTITITIGYGHAAPTDGGKVFQCFYALLGLPTLI 120
Db :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|: 123
64 LVLIQSEPHRAGVQWKPAGSFYFALTITITIGYGHAAPTDAGKAFQCFYAVLGLPTLI 123
QY 121 MFQSLGERINTFVRYLLHRAKGLGMRAEVSMMANVLIGFVSCISTLCIGAAAFSYER 180
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 183
124 MFQSLGERMTFVRYLLKRIKKCCGRNVDVSMENVTVGFFSCMGTLTCIGAAAFSQCEE 183
QY 181 WTFPOAYYCFITLTITIGFDYVALQDQALQTOQYVAFSFVYILTGLTVIGAFNLV 240
Db :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|: 243
184 WSFFHAYTYCFITLTITIGFDYVALQTKGALQKPLVYAFSPMYILVGLTVIGAFNLV 243
QY 241 LRFMTWNAEDEKRAEHRALLTHNGQAVLGGSLGSLGVDVRPRDPVTCAAAAGGVG 300
Db :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|: 284
244 LRLFTWSEDERDAERASLAGNRN-----SWVIHPEPRFSRP----- 284
QY 301 GVGSGFRNVYAEVLHFOFSCSCLWYKREKLQYSIPMIIPRDLSTSDTCVHSHS---- 356
Db :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|: 333
285 -----RYKADVPLQSVCSCTCYRQD---YGERSVAPQNSFSAKLAPHYFHSISYK 333
QY 357 -----SPGGGRYSDTSPHPCSCGTORGSAISSVSTGLHSLAARGLMKRRSV 405
Db :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|: 374
334 IBEISPS-----TLKNSLPSPSSVSPGLSHFTDKHRLMKRRKSV 374

RESULT 9
CIW9_CAVPO
ID CIW9_CAVPO STANDARD; PRT; 365 AA.
AC Q9JL58;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium channel subfamily K member 9 (Acid-sensitive potassium
channel protein TASK-3) (TWIK-related acid-sensitive K+ channel 3).
GN Name=KCNK9; Synonyms=TASK3;
OS Cavia porcellus (Guinea pig).

CC	-1- FUNCTION:	Probable potassium channel subunit. No channel activity observed in heterologous systems. May need to associate with another protein to form a functional channel.
CC	-1- SUBUNIT:	Heterodimer (Potential).
CC	-1- SUBCELLULAR LOCATION:	Integral membrane protein.
CC	-1- TISSUE SPECIFICITY:	Brain-specific. Highly expressed in auditory nuclei, in Purkinje cells and in olfactory bulb mitral cells.
CC	-1- PTM:	Phosphorylated (Potential).
CC	-1- SIMILARITY:	Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.
CC	-----	
CC	This SWISS-PROT entry is copyright.	It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/ or send an email to license@isb-sib.ch).
CC	-----	
DR	EMBL;	AF467250; AAL77036.1; -;
DR	EMBL;	AF294353; AAK97094.1; -;
DR	RGD;	619733; Kcnk15.
DR	InterPro;	IPR005821; Ion trans.
DR	InterPro;	IPR003280; K+channel_2pore.
DR	InterPro;	IPR001622; K+channel_pore.
DR	InterPro;	IPR008073; TASK5_channel.
DR	InterPro;	IPR003092; TASK_channel.
DR	Pfam;	PF00520; Ion trans; 1.
DR	PRINTS;	PR01333; 2FOREKCHANNEL.
DR	PRINTS;	PR01690; TASK5CHANNEL.
DR	PRINTS;	PR01095; TASKCHANNEL.
KW	Ion transport; Ionic channel; Potassium channel;	
KW	Transmembrane; Transport; Voltage-gated channel.	
FT	DOMAIN 1	8 Cytoplasmic (Potential).
FT	TRANSMEM 9	29 Potential.
FT	DOMAIN 80	101 Pore-forming 1 (Potential).
FT	TRANSMEM 108	128 Potential.
FT	DOMAIN 129	158 Cytoplasmic (Potential).
FT	TRANSMEM 159	179 Potential.
FT	DOMAIN 189	209 Pore-forming 2 (Potential).
FT	TRANSMEM 223	243 Potential.
FT	DOMAIN 244	318 Cytoplasmic (Potential).
FT	CONFLICT 315	315 R -> W (in Ref. 2).
SQ	SEQUENCE	318 AA; 35651 MW; A0629212F56834ED CRC64;
Query Match 42.1%; Score 886.5; DB 1; Length 318;		
Best Local Similarity 66.0%; Pred. No. 1.6e-60;		
Matches 175; Conservative 32; Mismatches 57; Indels 1; Gaps 1;		
QY	1	ENVRTIALIVCTFTYLLVGAAVFDALSESPEMIERQRLRQLELRARNYLSGGYEELE 60
DB	4	QSARTAAILCILSYLLVGAAVFDALSESAERSRQRLARKRGEKRRKFSADDYRELE 63
QY	61	RVVLRLKPKHAGVQWRPAGSFPAITVITIGYGHAAAPSTDGKGKVCFMFALLIGIPLTLI 120
DB	64	RLALQAEPRHAGRQWRPAGSFPAITVITIGYGHAAAPSTDGKGKVCFMFALLIGIPLTIV 123
QY	121	MQOSLGERINTFVRYLLHRAKGLGMRHAEVSMANMVLIGFVSCISFLICGAAAFSYER 180
DB	124	TFOSLGERLNALVRCULLAAKRCIGURPHVSAENMVMVAGLLLCATLALGAAPFAHFEG 183
QY	181	WTFPQAYYYCFITLTITIGFDYVALQDQALQTPQPVAFSPFVYILTGLTVIGAFNLVV 240
DB	184	WTFPQAYYYCFITLTITIGFDYVALQDQALQKPPYVAFSFLYLLGLTVIGAFNLVV 243
QY	241	LRPMTWNADEKDAEHRALLTHNG 265
DB	244	LRFLA-SAEAPERAALRRASVFRRG 267
RESULT 14		
CIWF_HUMAN		
ID	CIWF_HUMAN	STANDARD; PRT; 330 AA.


```
QY 182 TFFQAYYYCITLTTTIGFDYVALQDQALQTOQYVAFSVVILTLGLTVIGAFNLVVL 241
DB 185 TFFHAYYYCITLTTTIGFDYVALQDQALQKLPYVAFSFLYLLGLTVIGAFNLVVL 244
QY 242 RFTMTNAEDKRD-----EHRALLTHNQAVGLGGLS-----CLSGSL 280
DB 245 RFLVASADWFERAARPPSPPPGAPESRGWLPRPARSVGSASVFCVHVKLERCARDNL 304
QY 281 GDVVRPRDPVTCAAAGGVGVGGSGGPR 308
DB 305 GFSPSPSP-----GVVGGQAPR 322

RESULT 15
O17185 PRELIMINARY; PRT; 329 AA.
AC O17185; O76795;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Suppressor protein 9 (Putative potassium channel subunit n2p38) (Two-
DE pore K+ channel).
GN Name=sup-9; ORFNames=F34D6.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium." ;
RL Science 282:2012-2018 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Murray J., Wohldmann P., O'Neal D.;
RT "The sequence of C. elegans cosmid F34D6." ;
RN Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA Wang Z.-W., Salkoff L.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE=22896676; PubMed=14534247;
RA de la Cruz I.P., Levin J.Z., Cummins C., Anderson P., Horvitz H.R.;
RT "sup-9, sup-10, and unc-93 may encode components of a two-pore K+
RT channel that coordinates muscle contraction in Caenorhabditis
RT elegans." ;
RL J. Neurosci. 23:9133-9145 (2003).
RN [8]
RP SEQUENCE FROM N.A.
RA Perez de la Cruz I., Horvitz H.R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the two pore domain potassium channel
```

```
CC (TC 1.A.1.8) family.
DR EMBL; AF025454; AAC71151.2; -.
DR EMBL; AF083652; AAC32863.1; -.
DR EMBL; AY357729; AAQ84518.1; -.
DR PIR; T32347; T32347.
DR PIR; T43509; T43509.
DR WormBase; WBGene00006318; sup-9.
DR WormPep; F34D6.3; CE28297.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0005216; F-ion channel activity; IEA.
DR GO; GO:0005267; F-potassium channel activity; IEA.
DR GO; GO:0006811; P-ion transport; IEA.
DR GO; GO:0006813; P-potassium ion transport; IEA.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR003280; K+channel 2pore.
DR InterPro; IPR001622; K+channel pore.
DR InterPro; IPR003092; TASK channel.
DR Pfam; PF00520; Ion trans_1.
DR PRINTS; PR01333; 2FOREKCHANNEL.
DR PRINTS; PR01095; TASKCHANNEL.
KW Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 329 AA; 36992 MW; 338A6D9A577464CD CRC64;

Query Match 38.0%; Score 800; DB 2; Length 329;
Best Local Similarity 47.8%; Pred. NO. 8.5e-54;
Matches 175; Conservative 51; Mismatches 82; Indels 58; Gaps 10;

QY 1 ENVRTLALIVCTFTYLLVGAAVFDALSEPEMERORLELRQLELRARNVLSGGYEELE 60
DB 4 QNIRTLISLVCTLTLLVGAAVFDALSETENEILQRLKVRREKLTKNMKNADYEILE 63
QY 61 RVVLRKPKHAGVQWRPAGSFYPAITVITTTIGYGHAA PSTDGGKVFVALLGIPLTLI 120
DB 64 ATIVKSVPHKAGYQWKFSGAFYFATVITTTIGYGHSTPMTDAGKVFCLYALAGIPLGLI 123
QY 121 MFOSLGERINTFVRYLLHRAKGLGMRHAEVSNMNVLLIGFVSCISTLCI--GAAAFSY 178
DB 124 MFOSIGERMNTFAAKLLRFRRAAG-KQPIVTSDDLII--FTGMGGLLIFGAFMFSSY 180
QY 179 ERWTFQAYYYCITLTTTIGFDYVALQDQALQTOQYVAFSVVILTLGLTVIGAFNL 238
DB 181 ENWTFYDVAYYCFVTLTTTIGFDYVALQKRGSLQTOPEYVFFSLVFLFGLTVISAAMNL 240
QY 239 VVLRFTMTNAEDKRDAEHRALLTHNQAVGLGGLSCLSGSLGDVVRPRDPVTCAAAGGV 298
DB 241 LVLRFLTMNTEDERRD-EQEAILAAG-LVRVGDPTA-DDDFGRLPLSDNVSLAS----- 292
QY 299 GVGVGSGGFRNVYAEVLHFQSMCSCSLWYKSREKLOYISIPMIIPRDLSTSDTCVEH---SH 355
DB 293 -----YQLP-----DEKLRRHRKH 310
QY 356 SSPGGG 361
DB 311 TEPHGG 316

Search completed: September 15, 2005, 23:01:10
Job time : 175 secs
```

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2005, 22:40:33 ; Search time 167 Seconds
(without alignments)
937.952 Million cell updates/sec

Title: US-09-939-483-5
Perfect score: 2105
Sequence: 1 ENVTALIVCTFTYLLVGA.....STGLHSLAARFGLMKRRSSV 405

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2105	100.0	405	3	Aay95230 Mouse pot
2	2065.5	98.1	412	8	Adi27916 Rat prote
3	1819	86.4	394	3	Aae10343 Murine TA
4	1819	86.4	394	3	Aay79674 Human sig
5	1819	86.4	394	3	Aay87291 Human pro
6	1819	86.4	394	8	Adi27924 Human pro
7	1819	86.4	394	8	Adi27925 Human pro
8	1819	86.4	394	8	Adi27915 Human pro
9	1404	66.7	309	4	Aau07620 Mouse 2p
10	1100	52.3	374	3	Aab18807 Amino aci
11	1100	52.3	374	3	Aab18813 Protein e
12	1100	52.3	374	4	Aag63338 Amino aci
13	1100	52.3	374	5	Aae13279 Human tra
14	1100	52.3	374	5	Aae22389 Human tra
15	1100	52.3	374	8	Adi27948 Human TWI
16	1100	52.3	376	8	Adi66129 Human pro
17	1100	52.3	376	8	Adi66471 Human pro
18	836.5	39.7	330	7	Adb80478 Ovarian C
19	836.5	39.7	400	4	Aae10679 Human TWI
20	836.5	39.7	400	8	Adi27912 Human TWI
21	828.5	39.4	330	4	Aab47334 FCTR11. 8
22	828.5	39.4	330	7	Adk18422 Human NOV
23	828.5	39.4	400	4	Aae10678 Human TWI
24	828.5	39.4	400	5	Aae13286 Human tra
25	828.5	39.4	400	8	Adi27909 Human TWI

26	779.5	37.0	436	4	ABG29273	Novel hum
27	768	36.5	279	4	AAMI4676	Peptide #
28	768	36.5	279	4	ABB33636	Peptide #
29	768	36.5	279	4	AAM27095	Peptide #
30	768	36.5	279	4	ABB28454	Peptide #
31	768	36.5	279	4	ABB19091	Protein #
32	768	36.5	279	4	AAM66810	Human bon
33	768	36.5	279	4	AAM54409	Human bra
34	768	36.5	279	4	ABG48478	Human liv
35	768	36.5	279	4	AAM02399	Peptide #
36	768	36.5	279	5	ABG36465	Human pep
37	753	35.8	340	4	ABB64375	Drosophil
38	752.5	35.7	408	4	AAB31804	Amino aci
39	726.5	34.5	398	4	ABB71787	Drosophil
40	610	29.0	212	6	ABO14995	Human NOV
41	369	17.5	491	8	ABO84626	Mouse can
42	364.5	17.3	292	5	AAU99894	Mouse pot
43	362.5	17.2	534	5	AAU81355	Novel hum
44	361.5	17.2	408	8	ABO84627	Human can
45	359	17.1	292	5	AAU99893	Rat potas

ALIGNMENTS

RESULT 1
AAY95230
ID AAY95230 standard; protein; 405 AA.
XX AC AAY95230;
XX AC AAY95230;
DT 29-AUG-2000 (first entry)
XX XX
DE Mouse potassium channel TASK.
XX XX
KW TASK; TWIK-related acid-sensitive K+ channel; mouse; potassium channel;
KW drug screening; hypertension; hypotensive; epilepsy; arrhythmia;
KW vascular diseases; neurodegenerative disease; ischaemia; anoxia;
KW endocrine disease; muscle disease; therapy.
XX OS Mus musculus.
XX XX
FH Key Location/Qualifiers
FT Modified-site 50 /note= "N-glycosylated"
FT Modified-site 334 /note= "O-phosphorylated"
FT Modified-site 403 /note= "O-phosphorylated"
FT Modified-site 404 /note= "O-phosphorylated"
WO200027871-A2.
PD 18-MAY-2000.
XX XX
PF 09-NOV-1999; 99WO-IB001886.
XX XX
PR 09-NOV-1998; 98US-0107692P.
PR 08-NOV-1999; 99US-00436265.
XX XX
PA (CNRS) CNRS CENT NAT RECH SCI.
XX XX
PI Duprat F, Lesage F, Lazdunski M;
XX XX
DR WPI; 2000-376487/32.
XX XX
PT New nucleic acid encoding a non-inactivating outwardly rectifying
PT potassium transport channel, designated TASK2, useful in the treatment of
PT hypertension or dysfunctions of the kidney, liver or pancreas.
XX PS Disclosure; Fig 8; 91pp; English.
XX XX

CC The present sequence is that of murine TASK (TWIK-related acid-sensitive
 CC K⁺ channel), a member of a new family of 2p domain potassium channels,
 CC also including human TWIK-1 (see AAY79673), human TASK1 (see AAY79674),
 CC and novel human TASK2 (see AAY79675). Human and mouse TASK proteins share
 CC 85% identity, indicating that they are products of orthologous genes. Host
 CC cells expressing TWIK-1 family members can be used to screen for
 CC substances that modulate the activity of members of the TWIK-1 family of
 CC potassium channels. The drugs identified may be useful in the treatment
 CC of diseases of the heart or of the nervous system, such as epilepsy,
 CC arrhythmia, vascular diseases, neurodegenerative diseases, kidney, liver
 CC or pancreas diseases, hypertension, diseases associated with ischaemia or
 CC anoxia, endocrine diseases associated with anomalies of hormone
 CC secretion, and muscle diseases

XX Sequence 405 AA;

Query Match 100.0%; Score 2105; DB 3; Length 405;
 Best Local Similarity 100.0%; Pred. No. 2,7e-224;
 Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENVRTALIVCTFTYLLVGAADFALSEPEMERORLELRQLELRARYNLSEGGVEELE 60
 DB 1 ENVRTALIVCTFTYLLVGAADFALSEPEMERORLELRQLELRARYNLSEGGVEELE 60

QY 61 RVVLRKPKHAGVQWRPAGSFYFAITVTTTIGYGHAAAPSTDGKGVFCMFYALLGIPLTLI 120
 DB 61 RVVLRKPKHAGVQWRPAGSFYFAITVTTTIGYGHAAAPSTDGKGVFCMFYALLGIPLTLI 120

QY 121 MFQSLGERINTFVRYLLHRAKRGGLGMRHAEVSMANVLIQVSCISTLCIGAAAFSYFER 180
 DB 121 MFQSLGERINTFVRYLLHRAKRGGLGMRHAEVSMANVLIQVSCISTLCIGAAAFSYFER 180

QY 181 WTEFQAYYCFITLTITGFGDYVALQDQALQTOQYVAFSFVYILGLTVIGAFNLV 240
 DB 181 WTEFQAYYCFITLTITGFGDYVALQDQALQTOQYVAFSFVYILGLTVIGAFNLV 240

QY 241 LRFMTMAEDKRAEHRALLTHNGQAVGLGSLGSLGSDVPRDPVTCMAAGGVGV 300
 DB 241 LRFMTMAEDKRAEHRALLTHNGQAVGLGSLGSLGSDVPRDPVTCMAAGGVGV 300

QY 301 GVGSGFRNVYAEVLHFQSMCCLWYKREKLOYISPMIIPRDLSTSDTCVEHSHSPGG 360
 DB 301 GVGSGFRNVYAEVLHFQSMCCLWYKREKLOYISPMIIPRDLSTSDTCVEHSHSPGG 360

QY 361 GGRYSDFPSHPCSLGSGTQRSASISVSTGLHSLAAPRGLMKRRSSV 405
 DB 361 GGRYSDFPSHPCSLGSGTQRSASISVSTGLHSLAAPRGLMKRRSSV 405

RESULT 2

ID ADI27916

XX ADI27916 standard; protein; 412 AA.

AC ADI27916;

XX 06-MAY-2004 (first entry)

DT Rat protein #1.

DE Rat; ion channel family; ICF; cancer; leukaemia; Alzheimer's disease;
 XX Parkinson's disease; multiple sclerosis; epilepsy; hepatic disorder;
 KW cardiovascular disorder; cytostatic; neuroprotective; nootropic;
 KW antiparkinsonian; hepatotropic; cardiovascular.
 XX Rattus norvegicus.
 XX US2003165891-A1.
 XX 04-SEP-2003.
 XX 15-MAY-2002; 2002US-00146733.
 XX 29-FEB-2000; 2000US-00515520.

PR 29-FEB-2000; 2000US-0185938P.
 PR 03-MAR-2000; 2000US-00518866.
 PR 07-APR-2000; 2000US-0195734P.
 PR 11-APR-2000; 2000US-0195993P.
 PR 26-APR-2000; 2000US-0199799P.
 PR 19-SEP-2000; 2000US-0233537P.
 PR 25-SEP-2000; 2000US-0235018P.
 PR 25-SEP-2000; 2000US-0235059P.
 PR 15-DEC-2000; 2000US-0256240P.
 PR 18-DEC-2000; 2000US-0256588P.
 PR 21-DEC-2000; 2000US-0258028P.
 PR 28-FEB-2001; 2001US-00796720.
 PR 06-APR-2001; 2001US-00828035.
 PR 11-APR-2001; 2001US-00833081.
 PR 25-APR-2001; 2001US-00843128.
 PR 19-SEP-2001; 2001US-00957683.
 PR 25-SEP-2001; 2001US-00964252.
 PR 25-SEP-2001; 2001US-00964256.
 PR 17-DEC-2001; 2001US-00024623.
 XX (MILL-) MILLENNIUM PHARM INC.
 PA Curtis RAJ, Glucksmann MA, Silos-Santiago I;
 PI WPI; 2004-069000/07.
 XX

XX Disclosure; SEQ ID NO 9; 638pp; English.

XX The invention relates to TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611,
 CC IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and 53763 ion channel
 CC family (ICF) nucleic acids and proteins. The TWIK-6, TWIK-7, IC23927,
 CC TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and
 CC 53763 ICF nucleic acids and proteins may be used for preventing,
 CC diagnosing and treating ICF-related diseases. The sequences may be used
 CC to treat disorders associated with decreased expression by rectifying of
 CC mutations or deletions in a patient's genome that affect the activity of
 CC ICF proteins by expressing inactive proteins or to supplement the
 CC patients own production of ICF proteins. The proteins may also be used as
 CC antigens in the production of antibodies against ICF proteins and in
 CC assays to identify modulators of ICF protein expression and activity. The
 CC anti-ICF protein antibodies, agonists and antagonists may be used to
 CC regulate ICF protein expression and activity. The antibodies may also be
 CC used as diagnostic agents for detecting the presence of ICF proteins in
 CC samples (e.g. by immunoassay). The nucleic acids and proteins may be used
 CC to prevent, diagnose and treat a wide variety of disorders, e.g. cancers.
 CC and leukaemia, Alzheimer's disease, Parkinson's disease, multiple
 CC sclerosis, epilepsy, hepatic disorders and cardiovascular disorders. This
 CC sequence represents a rat protein used in the scope of the invention.
 CC Note: The sequence data for this patent is also available in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 412 AA;

Query Match 98.1%; Score 2065.5; DB 8; Length 412;
 Best Local Similarity 98.0%; Pred. No. 6,7e-220;
 Matches 400; Conservative 3; Mismatches 2; Indels 3; Gaps 2;

QY 1 ENVRTALIVCTFTYLLVGAADFALSEPEMERORLELRQLELRARYNLSEGGVEELE 60
 DB 5 QNVRTALIVCTFTYLLVGAADFALSEPEMERORLELRQLELRARYNLSEGGVEELE 64

QY 61 RVVLRKPKHAGVQWRPAGSFYFAITVTTTIGYGHAAAPSTDGKGVFCMFYALLGIPLTLI 120
 DB 65 RVVLRKPKHAGVQWRPAGSFYFAITVTTTIGYGHAAAPSTDGKGVFCMFYALLGIPLTIV 124

QY 121 MFQSLGERINTFVRYLLHRAKRGGLGMRHAEVSMANVLIQVSCISTLCIGAAAFSYFER 180
 DB 125 MFQSLGERINTFVRYLLHRAKRGGLGMRHAEVSMANVLIQVSCISTLCIGAAAFSYFER 184

QY 181 WTFQAYYYCFITLTTIGFDYVALQKQALOTQYVAFSVYILTLTGLTVIGAFNLV 240
 DB 185 WTFQAYYYCFITLTTIGFDYVALQKQALOTQYVAFSVYILTLTGLTVIGAFNLV 244
 QY 241 LRFMTNAEDEKRAEHRALLTHNGQAVGLGGLSCLSGSLGD-VPRDPVTCAAAAG--G 297
 DB 245 LRFMTNAEDEKRAEHRALLTHNGQAGLGLSCLSGSLGDVGRPRDPVTCAAAAGMG 304
 QY 298 VGVGGSGFRNVYAEVLHFQSMCCLWYKSREKLQYSIPMIIPRDLSTSDTCVEHSHSS 357
 DB 305 VGVGGSGFRNVYAEVLHFQSMCCLWYKSREKLQYSIPMIIPRDLSTSDTCVEHSHSS 364
 QY 358 PGCGGRYSDTPSHPCLCGTQRSALSSVSTGLHSLAARFGLMKRRSSV 405
 DB 365 PGCGGRYSDTPSHPCLCGTQRSALSSVSTGLHSLATFRGLMKRRSSV 412

RESULT 3
 AAE10343
 ID AAE10343 standard; protein; 394 AA.
 XX
 AC AAE10343;
 XX
 DT 10-DEC-2001 (first entry)
 XX
 DE Murine TASK potassium channel protein.
 XX
 KW Murine; potassium channel protein; TREK-1; TASK; anaesthetic; analgesia;
 KW amnesia.
 XX
 OS Mus sp.
 XX
 PN WO200047738-A2.
 XX
 PD 17-AUG-2000.
 XX
 PF 11-FEB-2000; 2000WO-IB000226.
 XX
 PR 12-FEB-1999; 99US-0119727P.
 PR 11-FEB-2000; 2000US-00503089.
 XX
 PA (CNRS) CNRS CENT NAT RECH SCI.
 XX
 PI Lazdunski M, Honore E, Lesage F, Romey G, Patel AJ;
 XX
 XX WPI; 2000-549146/50.
 XX
 DR Novel nucleic acid encoding a TREK-1 potassium channel protein for
 PT transfecting cells to be used to identify compounds with anesthetic
 PT properties.
 XX
 PS Claim 23; Page 34-35; 39pp; English.
 XX
 CC The invention relates to human and mouse TREK-1 potassium channel
 CC proteins and their corresponding DNA molecules. TREK-1 nucleic acid is
 CC useful for transfecting cells to induce expression of the TREK-1
 CC potassium channel protein. These cells are then used in assays to
 CC identify compounds which have anaesthetic properties, producing a safe,
 CC reversible state of unconsciousness with concurrent amnesia and analgesia
 CC in a mammal upon inhalation. The present sequence is murine TASK
 CC potassium channel protein related to the invention
 XX
 SQ Sequence 394 AA;
 Query Match 86.4%; Score 1819; DB 3; Length 394;
 Best Local Similarity 88.1%; Pred. No. 1.5e-192;
 Matches 357; Conservative 9; Mismatches 25; Indels 14; Gaps 2;
 QY 1 ENVRTALIVCTFTYLLVGAAVFDALSEPEMERQRLERQLELRARYNLSEGGYELE 60
 DB 4 QNVRTALIVCTFTYLLVGAAVFDALSEPEMERQRLERQLELRARYNLSEGGYELE 63

QY 61 RVVLRKPKKAGVQWRFAGSFYFAITVTTTIGYHAAPSTDGKVFQCMFYALLGIPLTLLI 120
 DB 64 RVVLRKPKKAGVQWRFAGSFYFAITVTTTIGYHAAPSTDGKVFQCMFYALLGIPLTLLV 123
 QY 121 MFQSLGRINTFVYLLHRAKRGMRHAESVMANMVLIGFVSCISTLCIGAAAFAFVYER 180
 DB 124 MFQSLGRINTFVYLLHRAKRGMRADVSMANMVLIGFVSCISTLCIGAAAFAFVYEH 183
 QY 181 WTFQAYYYCFITLTTIGFDYVALQKQALOTQYVAFSVYILTLTGLTVIGAFNLV 240
 DB 184 WTFQAYYYCFITLTTIGFDYVALQKQALOTQYVAFSVYILTLTGLTVIGAFNLV 243
 QY 241 LRFMTNAEDEKRAEHRALLTHNGQAVGLGGLSCLSGSLGDVPRDPVTCAAAAGGVGV 300
 DB 244 LRFMTNAEDEKRAEHRALLTRNGQAGGGG-----GSAHTTDTASTNAA----- 291
 QY 301 GVGSGFRNVYAEVLHFQSMCCLWYKSREKLQYSIPMIIPRDLSTSDTCVEHSHSSPGG 360
 DB 292 --GGGFRNVYAEVLHFQSMCCLWYKSREKLQYSIPMIIPRDLSTSDTCVEHSHSSPGG 349
 QY 361 GGRYSDTPSHPCLCGTQRSALSSVSTGLHSLAARFGLMKRRSSV 405
 DB 350 GGRYSDTPSHPCLCGTQRSALSSVSTGLHSLATFRGLMKRRSSV 394

RESULT 4
 AAY79674
 ID AAY79674 standard; protein; 394 AA.
 XX
 AC AAY79674;
 XX
 DT 29-AUG-2000 (first entry)
 XX
 DE Human potassium channel TASK1.
 XX
 KW TASK1; TWIK-related acid-sensitive K+ channel 1; human;
 KW potassium channel; drug screening; hypertension; hypotensive; epilepsy;
 KW arrhythmia; vascular diseases; neurodegenerative disease; ischaemia;
 KW anoxia; endocrine disease; muscle disease; therapy.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT Modified-site 53 /note= "N-glycosylated"
 FT Modified-site 323 /note= "O-phosphorylated"
 FT Modified-site 383 /note= "O-phosphorylated"
 FT Modified-site 392 /note= "O-phosphorylated"
 FT Modified-site 393 /note= "O-phosphorylated"
 FT Modified-site 393 /note= "O-phosphorylated"
 XX
 PN WO200027871-A2.
 XX
 PD 18-MAY-2000.
 XX
 PF 09-NOV-1999; 99WO-IB001886.
 XX
 PR 09-NOV-1998; 98US-0107692P.
 PR 08-NOV-1999; 99US-00436265.
 XX
 PA (CNRS) CNRS CENT NAT RECH SCI.
 XX
 PI Duprat F, Lesage F, Lazdunski M;
 XX
 DR WPI; 2000-376487/32.
 DR N-PSDB; AAA27746.
 XX
 PT New nucleic acid encoding a non-inactivating outwardly rectifying
 PT potassium transport channel, designated TASK2, useful in the treatment of
 PT hypertension or dysfunctions of the kidney, liver or pancreas.

```
XX Disclosure; Fig 8; 91pp; English.
XX
XX The present sequence is that of human TASK1 (TWIK-related acid-sensitive
CC K+ channel), a member of a new family of 2p domain potassium channels,
CC also including TWIK-1 (see AA79673) and novel TASK2 (see AA79675).
CC TASK1 is expressed in many different tissues, and at particularly high
CC levels in pancreas and placenta. Host cells expressing TWIK-1 family
CC members can be used to screen for substances that modulate the activity
CC of members of the TWIK-1 family of potassium channels. The drugs
CC identified may be useful in the treatment of diseases of the heart or of
CC the nervous system, such as epilepsy, arrhythmia, vascular diseases,
CC neurodegenerative diseases, kidney, liver or pancreas diseases,
CC hypertension, diseases associated with ischaemia or anoxia, endocrine
CC diseases associated with anomalies of hormone secretion, and muscle
XX diseases
XX
XX Sequence 394 AA;
SQ
    Query Match      86.4%; Score 1819; DB 3; Length 394;
    Best Local Similarity 88.1%; Pred. No. 1.5e-192;
    Matches 357; Conservative 9; Mismatches 25; Indels 14; Gaps 2;

QY 1 ENVRTALIVCTFTYLLVGAADFDALESEPEMERQRLERQLELRARYNLSGGYBELE 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4 QNVRTALIVCTFTYLLVGAADFDALESEPEMERQRLERQLELRARYNLSGGYBELE 63

QY 61 RVVLRKPKHKGAVQWRPAGSFYFAITVTTIGYGHAAAPSTDGKVFQCMFYALLGIPLTLI 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
64 RVVLRKPKHKGAVQWRPAGSFYFAITVTTIGYGHAAAPSTDGKVFQCMFYALLGIPLTIV 123

QY 121 MFQSLGERINTFVRYLLHRAKGLGMRHAESVMANMVLIGFVSCITLCIGAAAFSYHER 180
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
124 MFQSLGERINTLVRYLLHRAKGLGMRADVSMANMVLIGFVSCITLCIGAAAFSHEYH 183

QY 181 WTFQAYYYCFTITLTIGFGDYVALQDQALQTOPOQYVAFSVYLTGLTVIGAFNLV 240
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
184 WTFQAYYYCFTITLTIGFGDYVALQDQALQTOPOQYVAFSVYLTGLTVIGAFNLV 243

QY 241 LRFVTMAEDBKRAEHRALLTHNGOAVGLGSLGSLDVRPRPVTCAAAAGGVGV 300
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
244 LRFVTMAEDBKRAEHRALLTRNGAGGGG-----GGSAHTDTASTAAA----- 291

QY 301 GVGSGFRNVYAEVLHFQSMCSCLWYKSREKLOYSIPMIIPRDLSTSDTCVEHSHSPGG 360
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
292 --GGGGRNVYAEVLHFQSMCSCLWYKSREKLOYSIPMIIPRDLSTSDTCVEHSHSPGG 349

QY 361 GGRVSDTPSHCLSGTORSIAISSVSTGLHSLAARGLMKRRSSV 405
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
350 GGRVSDTPSHCLSGAPRSIAISSVSTGLHSLSTFRGLMKRRSSV 394

RESULT 5
AA87291
ID AA87291 standard; protein; 394 AA.
XX
XX AA87291;
XX
XX 11-MAY-2000 (first entry)
XX
XX Human signal peptide containing protein HSP-68 SEQ ID NO:68.
XX
XX Human; signal peptide-containing protein; HSP; diagnosis; cancer;
XX inflammation; cardiovascular disease; anticancer; anti-inflammatory;
XX antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic;
XX antiasthmatic; gene therapy; cell proliferation; neurological disorder;
XX reproductive disorder; developmental disorder; arteriosclerosis;
XX cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
XX asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
XX Parkinson's disease; Huntington's diseases; ovulatory defect;
XX muscular dystrophy.
XX
XX Homo sapiens.
OS
```

```
XX WO200000610-A2.
XX
XX 06-JAN-2000.
XX
XX 25-JUN-1999; 99WO-US014484.
XX
XX 26-JUN-1998; 98US-0090762P.
XX 31-JUL-1998; 98US-0094983P.
XX 01-OCT-1998; 98US-0102686P.
XX 11-DEC-1998; 98US-0112129P.
XX (INCY-) INCYTE PHARM INC.
XX
XX Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
XX Akerman IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
XX Bandman O;
XX
XX WPI; 2000-160673/14.
XX N-PSDB; AA298176.
XX
XX New human signal peptide-containing proteins useful in treatment,
XX prevention and diagnosis of e.g. cancer, inflammation and cardiovascular
XX disease.
XX
XX Claim 1; Page 207-208; 327pp; English.
XX
XX AA298109 to AA298242 encode AA87224 to AA87357 which represent the
XX human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have
XX anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic,
XX neuroprotective, cardiovascular and antiasthmatic activities, and can be
XX used in gene therapy. HSPs can be used to treat or prevent disorders
XX associated with decreased activity or function of HSP. Antagonists of
XX HSP are used to treat or prevent disorders associated with increased
XX activity or function of HSP. Such diseases include cell proliferation
XX (including cancer), inflammation, cardiovascular, neurological,
XX reproductive or developmental disorders, (e.g. arteriosclerosis,
XX cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
XX asthma, Crohn's disease, microbial or other infections, congestive or
XX ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
XX diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSP
XX nucleic acids can be used for the recombinant production of HSP, for
XX detecting HSP in standard hybridisation and amplification assays (for
XX diagnosis and monitoring), in gene therapy, as antisense, triplex-forming
XX or ribozyme therapeutics, for detecting related sequences or genetic
XX variations, and for chromosomal mapping. HSP are also used to raise
XX specific antibodies (Ab) and to screen for agonists and antagonists
XX (potential therapeutic agents). Ab are used to diagnose, or monitor, HSP
XX -related diseases (in usual immunoassays), as therapeutic antagonists, in
XX competitive drug screens, and for purification of HSP from natural
XX sources
XX
XX Sequence 394 AA;
XX
    Query Match      86.4%; Score 1819; DB 3; Length 394;
    Best Local Similarity 88.1%; Pred. No. 1.5e-192;
    Matches 357; Conservative 9; Mismatches 25; Indels 14; Gaps 2;

QY 1 ENVRTALIVCTFTYLLVGAADFDALESEPEMERQRLERQLELRARYNLSGGYBELE 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4 QNVRTALIVCTFTYLLVGAADFDALESEPEMERQRLERQLELRARYNLSGGYBELE 63

QY 61 RVVLRKPKHKGAVQWRPAGSFYFAITVTTIGYGHAAAPSTDGKVFQCMFYALLGIPLTLI 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
64 RVVLRKPKHKGAVQWRPAGSFYFAITVTTIGYGHAAAPSTDGKVFQCMFYALLGIPLTIV 123

QY 121 MFQSLGERINTFVRYLLHRAKGLGMRHAESVMANMVLIGFVSCITLCIGAAAFSYHER 180
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
124 MFQSLGERINTLVRYLLHRAKGLGMRADVSMANMVLIGFVSCITLCIGAAAFSHEYH 183

QY 181 WTFQAYYYCFTITLTIGFGDYVALQDQALQTOPOQYVAFSVYLTGLTVIGAFNLV 240
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
184 WTFQAYYYCFTITLTIGFGDYVALQDQALQTOPOQYVAFSVYLTGLTVIGAFNLV 243
```

```
QY 241 LRFMTMNAEDEKRDHRAHLLTHNGOAVCLGSLGSLGVDVRPRDPVTCARAGGVGV 300
DB 244 LRFMTMNAEDEKRDHRAHLLTRNGOAGGGG-----GSAHTTDTASSTAAA----- 291
QY 301 GVGSGFRNVYAEVLHFQSMCCLWYKREKLYQSIPIPIPRDLSTSDTCVEHSHSSPGG 360
DB 292 --GGGGRNVYAEVLHFQSMCCLWYKREKLYQSIPIPIPRDLSTSDTCVEQSHSSPGG 349
QY 361 GGRYSDTPSHPCLCGQTSRQSAISSVSTGLHSLAARGLMKRRSSV 405
DB 350 GGRYSDTPSRRLCLSCGAPRSATSSVSTGLHSLSTRGLMKRRSSV 394

RESULT 6
ADI27924
ID ADI27924 standard; protein; 394 AA.
AC ADI27924;
XX 06-MAY-2004 (first entry)
XX Human protein #2.
XX Human; ion channel family; ICF; cancer; leukaemia; Alzheimer's disease;
KW Parkinson's disease; multiple sclerosis; epilepsy; hepatic disorder;
KW cardiovascular disorder; cytostatic; neuroprotective; nootropic;
KW antiparkinsonian; hepatotropic; cardiovascular.
XX Homo sapiens.
XX US2003165891-A1.
XX 04-SEP-2003.
XX 15-MAY-2002; 2002US-00146733.
XX 29-FEB-2000; 2000US-00515520.
XX 29-FEB-2000; 2000US-0185938P.
XX 03-MAR-2000; 2000US-00518866.
XX 07-APR-2000; 2000US-0195734P.
XX 11-APR-2000; 2000US-0195993P.
XX 26-APR-2000; 2000US-0193793P.
XX 19-SEP-2000; 2000US-0233537P.
XX 25-SEP-2000; 2000US-0235018P.
XX 25-SEP-2000; 2000US-0235059P.
XX 15-DEC-2000; 2000US-0256240P.
XX 18-DEC-2000; 2000US-0256588P.
XX 21-DEC-2000; 2000US-0258028P.
XX 28-FEB-2001; 2001US-00796720.
XX 06-APR-2001; 2001US-00828035.
XX 11-APR-2001; 2001US-00833081.
XX 25-APR-2001; 2001US-00843128.
XX 19-SEP-2001; 2001US-00957693.
XX 25-SEP-2001; 2001US-00964252.
XX 25-SEP-2001; 2001US-00964256.
XX 17-DEC-2001; 2001US-00024623.
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Curtis RAJ, Glucksmann MA, Silos-Santiago I;
XX WPI; 2004-069000/07.
XX
XX TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9,
PT alpha2delta-4, 54414, or 53763 nucleic acids and proteins, useful for
PT preventing, diagnosing and treating e.g. cancers, Alzheimer's disease and
PT cardiovascular disorders.
XX Disclosure; SEQ ID NO 17; 638pp; English.
XX
XX The invention relates to TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611,
CC IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and 53763 ion channel
```

```
CC family (ICF) nucleic acids and proteins. The TWIK-6, TWIK-7, IC23927,
CC TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and
CC 53763 ICF nucleic acids and proteins may be used for preventing,
CC diagnosing and treating ICF-related diseases. The sequences may be used
CC to treat disorders associated with decreased expression by rectifying
CC mutations or deletions in a patient's genome that affect the activity of
CC ICF proteins by expressing inactive proteins or to supplement the
CC patients own production of ICF proteins. The proteins may also be used as
CC antigens in the production of antibodies against ICF proteins and in
CC assays to identify modulators of ICF protein expression and activity. The
CC anti-ICF protein antibodies, agonists and antagonists may be used to
CC regulate ICF protein expression and activity. The antibodies may also be
CC used as diagnostic agents for detecting the presence of ICF proteins in
CC samples (e.g. by immunoassay). The nucleic acids and proteins may be used
CC to prevent, diagnose and treat a wide variety of disorders, e.g. cancers
CC and leukaemia, Alzheimer's disease, Parkinson's disease, multiple
CC sclerosis, epilepsy, hepatic disorders and cardiovascular disorders. This
CC sequence represents a human protein used in the scope of the invention.
CC Note: The sequence data for this patent is also available in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX SQ Sequence 394 AA;
XX Query Match 86.4%; Score 1819; DB 8; Length 394;
XX Best Local Similarity 88.1%; Pred. No. 1.5e-192;
XX Matches 357; Conservative 9; Mismatches 25; Indels 14; Gaps 2;
QY 1 ENVTALIVCTFTYLLVGAADFALSEPEMIERQLELRQLRLARYNLSEGGYBELE 60
DB 4 QNVTALIVCTFTYLLVGAADFALSEPEMIERQLELRQLRLARYNLSEGGYBELE 63
QY 61 RVLRLKPKHKGAVQVRFAGSFYFAITVITTTIGYGHAAAPSTDGGKVFYALLGIPLTLI 120
DB 64 RVLRLKPKHKGAVQVRFAGSFYFAITVITTTIGYGHAAAPSTDGGKVFYALLGIPLTIV 123
QY 121 MFQSLGERINTFVYLLHRAKRGIGMRHAEVSMANMVLIGFVSCISTLCIGAAAFSYVER 180
DB 124 MFQSLGERINTFVYLLHRAKRGIGMRADVSMANMVLIGFSCISTLCIGAAAFSHYEH 183
QY 181 WTFQAYYCFITLTTTIGFDYVALQDQALQTPQVAFSFVYILTGLTVIGAFNLVV 240
DB 184 WTFQAYYCFITLTTTIGFDYVALQDQALQTPQVAFSFVYILTGLTVIGAFNLVV 243
QY 241 LRFMTMNAEDEKRDHRAHLLTHNGOAVGLGGLSCLSGSLGVDVRPRDPVTCARAGGVGV 300
DB 244 LRFMTMNAEDEKRDHRAHLLTRNGOAGGGG-----GSAHTTDTASSTAAA----- 291
QY 301 GVGSGFRNVYAEVLHFQSMCCLWYKREKLYQSIPIPIPRDLSTSDTCVEHSHSSPGG 360
DB 292 --GGGGRNVYAEVLHFQSMCCLWYKREKLYQSIPIPIPRDLSTSDTCVEQSHSSPGG 349
QY 361 GGRYSDTPSHPCLCGQTSRQSAISSVSTGLHSLAARGLMKRRSSV 405
DB 350 GGRYSDTPSRRLCLSCGAPRSATSSVSTGLHSLSTRGLMKRRSSV 394

RESULT 7
ADI27925
ID ADI27925 standard; protein; 394 AA.
XX
XX AC ADI27925;
XX 06-MAY-2004 (first entry)
XX Human protein #3.
XX Human; ion channel family; ICF; cancer; leukaemia; Alzheimer's disease;
KW Parkinson's disease; multiple sclerosis; epilepsy; hepatic disorder;
KW cardiovascular disorder; cytostatic; neuroprotective; nootropic;
KW antiparkinsonian; hepatotropic; cardiovascular.
XX
XX Homo sapiens.
XX
```


Db 64 LVILQSEPHRAGVQWKFGSFYFAITVTITIGYGHAAFGTDAGKAFCMFYAVLGIPLTIV 123
Qy 121 MFQSLGERINTFVRYLLHRAKRGGLMRHAESVMANNVILGIFVSCISTLCIGAAAFSYYER 180
Db 124 MFQSLGERMNTFVRYLLKRIKCCGMNTDVSMMNMTVGFSCMGTLICIGAAAFSQCEE 183
Qy 181 WTPFOAYYCFITLTITIGFDYVALQKQALQTOQYVAFSPVYILTGLTVIGAFPLNLV 240
Db 184 WSPFHAYYCFITLTITIGFDYVALQKQALQKPLVAFSPMYTLVGLTVIGAFPLNLV 243
Qy 241 LRFMTMAEKRDAEHRALLTHNGQAVLGGLGSLGSDVPRDPTVTCAAAGGVGV 300
Db 244 LRLFTMNSDEKRDAAERASLAGNRN-----SMVTHIPEEPRSRP----- 284
Qy 301 GVGSGFRNVYAEVLHFQSMCCLWYKREKIQYSIPMIIPRDLSTSDTCVEHSHS----- 356
Db 285 -----RYKADVPDLQSVCSCTCYRSQD---YGRSVAPQNSFSKLAAPHYSISYK 333
Qy 357 ----SPGGGRYSDTPSHPCLCSTQRTSAISSVSTGLHSLAFAFGMLKRRSSV 405
Db 334 IEEISPS-----TLKNSLFPSPISISPLHSTFDHQRLMKRRKSV 374

RESULT 12
AAG63938
ID AAG63938 standard; protein; 374 AA.
AC AAG63938;
XX
XX
XX 29-OCT-2001 (first entry)
XX
XX Amino acid sequence of human potassium channel protein KCNB.
XX
XX Human; potassium channel protein; KCNB; breast tissue; cancer; stroke;
KW potassium channel-associated disorder; brain associated disorder;
KW epilepsy; Alzheimer's disease; Parkinson's disease; multiple sclerosis;
KW migraine; psychiatric disorder; depression; schizophrenia; diabetes;
KW bipolar disease; heart disease; arrhythmia; pancreas disease;
XX pancreatitis.
XX
OS Homo sapiens.
XX
XX WO200166741-A2.
XX
XX 13-SEP-2001.
XX
XX 02-MAR-2001; 2001WO-US006801.
XX
XX 03-MAR-2000; 2000US-0186915P.
XX
XX (TULA-) TULARIK INC.
XX
XX Mu D, Powers S;
PI
XX WPI; 2001-522949/57.
DR N-PSDB; AAH74999.
XX
XX A nucleic acid encoding a potassium channel, termed KCNB (potassium
PT channel expressed in breast), useful in the diagnosis, prognosis or
PT treatment of diseases associated with altered KCNB activity or
PT expression, e.g. cancer and diabetes.
XX
XX Claim 16; Page 79; 82pp; English.
XX
XX The present sequence represents a human potassium channel protein, termed
CC KCNB. KCNB is expressed in breast tissue. The KCNB polypeptides are
CC useful for identifying a compound that modulates its activity. The KCNB
CC polypeptide and nucleic acid are useful for detecting cancer cells in
CC biological samples. The inhibitor of the potassium channel polypeptide is
CC useful for inhibiting proliferation of a cancer cell and for treating a
CC potassium channel-associated disorder. The KCNB nucleic acids, proteins,
CC and/or antibodies are useful in the diagnosis or prognosis, or treatment

CC of diseases associated with altered KCNB activity or expression. Such
CC diseases are cancer, brain associated disorders (such as epilepsy,
CC Alzheimer's disease, Parkinson's disease, stroke, multiple sclerosis,
CC migraine), psychiatric disorders (such as depression, schizophrenia,
CC bipolar diseases) and diseases related to the heart (such as
CC arrhythmias), diseases related to pancreas (such as pancreatitis and
CC diabetes)
XX
SQ Sequence 374 AA;
Query Match 52.3%; Score 1100; DB 4; Length 374;
Best Local Similarity 55.48; Pred. No. 1.1e-112;
Matches 229; Conservative 48; Mismatches 86; Indels 50; Gaps 5;
Qy 1 ENVTALIVCTFTYLLVGAADFDALESEPEMTERQRLERLQLELRARNYNLSEGYEELE 60
Db 4 QNVRTLILVCTFTYLLVGAADFDALESDHEMREKXKABEIRIKGYNISSEDYRQLE 63
Qy 61 RVLRLPHKAGVQWRFAGSFYFAITVTITIGYGHAAFGTDGKAFCMFYAVLGIPLTIV 120
Db 64 LVILQSEPHRAGVQWKFGSFYFAITVTITIGYGHAAFGTDAGKAFCMFYAVLGIPLTIV 123
Qy 121 MFQSLGERINTFVRYLLHRAKRGGLMRHAESVMANNVILGIFVSCISTLCIGAAAFSYYER 180
Db 124 MFQSLGERMNTFVRYLLKRIKCCGMNTDVSMMNMTVGFSCMGTLICIGAAAFSQCEE 183
Qy 181 WTPFOAYYCFITLTITIGFDYVALQKQALQTOQYVAFSPVYILTGLTVIGAFPLNLV 240
Db 184 WSPFHAYYCFITLTITIGFDYVALQKQALQKPLVAFSPMYTLVGLTVIGAFPLNLV 243
Qy 241 LRFMTMAEKRDAEHRALLTHNGQAVLGGLGSLGSDVPRDPTVTCAAAGGVGV 300
Db 244 LRLFTMNSDEKRDAAERASLAGNRN-----SMVTHIPEEPRSRP----- 284
Qy 301 GVGSGFRNVYAEVLHFQSMCCLWYKREKIQYSIPMIIPRDLSTSDTCVEHSHS----- 356
Db 285 -----RYKADVPDLQSVCSCTCYRSQD---YGRSVAPQNSFSKLAAPHYSISYK 333
Qy 357 ----SPGGGRYSDTPSHPCLCSTQRTSAISSVSTGLHSLAFAFGMLKRRSSV 405
Db 334 IEEISPS-----TLKNSLFPSPISISPLHSTFDHQRLMKRRKSV 374
RESULT 13
AAE13279
ID AAE13279 standard; protein; 374 AA.
XX
XX AAE13279;
XX
XX 12-FEB-2002 (first entry)
XX
XX Human transporters and ion channels (TRICH)-6.
XX
XX Human; transporter and ion channel; TRICH; akinesia; cystic fibrosis;
KW diabetes mellitus; Parkinson's disease; myasthenia gravis; dementia;
KW cardiac disorder; angina; hypertension; myocarditis; hyperglycemia;
KW neurological disorder; Alzheimer's disease; cataract; infertility;
KW Wilson's disease; schizophrenia; Grave's disease; Addison's disease;
KW Huntington's disease; multiple sclerosis; meningitis; hypotensive;
KW cardiant; nootropic; neuroprotective; neuroleptic; ophthalmological;
KW antihydroid; anticonvulsant; goltre; antiinflammatory.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
FH Peptide 1..25
FT Peptide /label= Signal_peptide
FT Protein 26..374
FT Protein /note= "Human mature TRICH6 protein"
FT Domain 225..243
FT /label= Transmembrane_domain
XX
XX WO200177174-A2.

CC TWIK-8, IC47611, IC47615, HNMDA-7, TWIK-9, alpha-2delta-4, 54414 and
CC 53763 ICF nucleic acids and proteins may be used for preventing,
CC diagnosing and treating ICF-related diseases. The sequences may be used
CC to treat disorders associated with decreased expression by rectifying
CC mutations or deletions in a patient's genome that affect the activity of
CC ICF proteins by expressing inactive proteins or to supplement the
CC patients own production of ICF proteins. The proteins may also be used as
CC antigens in the production of antibodies against ICF proteins and in
CC assays to identify modulators of ICF protein expression and activity. The
CC anti-ICF protein antibodies, agonists and antagonists may be used to
CC regulate ICF protein expression and activity. The antibodies may also be
CC used as diagnostic agents for detecting the presence of ICF proteins in
CC samples (e.g. by immunosassay). The nucleic acids and proteins may be used
CC to prevent, diagnose and treat a wide variety of disorders, e.g. cancers
CC and leukaemia, Alzheimer's disease, Parkinson's disease, multiple
CC sclerosis, epilepsy, hepatic disorders and cardiovascular disorders. This
CC sequence represents the human TWIK-9 protein of the invention. Note: The
CC sequence data for this patent is also available in electronic format
CC USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 374 AA;

Search completed: September 15, 2005, 22:58:14
Job time : 172 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2005, 21:54:16 ; Search time 26 Seconds
(without alignments)
1162.803 Million cell updates/sec

Title: US-09-939-483-5
Perfect score: 2105
Sequence: 1 ENVRTALIVCTFYLLVGA.....STGLHSLAARGLMKRRSSV 405

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCITUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2105	100.0	405	3	US-09-144-914-5
2	1819	85.4	394	3	US-09-144-914-4
3	1100	52.3	388	4	US-09-949-016-7631
4	752.5	35.7	408	4	US-09-362-842-12
5	354	16.8	361	4	US-09-362-842-14
6	352.5	16.7	538	4	US-09-949-016-7001
7	352.5	16.7	558	4	US-09-949-016-7368
8	346	16.4	370	3	US-09-144-914-8
9	345	16.4	411	3	US-09-236-080-6
10	341	16.2	393	4	US-09-432-470-2
11	341	16.2	393	4	US-09-432-470-4
12	341	16.2	419	4	US-09-949-016-6913
13	341	16.2	440	4	US-09-949-016-7809
14	337	16.0	411	3	US-09-236-080-2
15	337	16.0	411	3	US-09-336-643A-83
16	334.5	15.9	336	3	US-08-749-816-2
17	334.5	15.9	336	3	US-09-144-914-2
18	319.5	15.2	499	4	US-09-561-763-2
19	319.5	15.2	499	4	US-09-431-367B-2
20	317.5	15.1	146	4	US-09-362-842-69
21	317.5	15.1	146	4	US-09-270-767-31685
22	310	14.7	995	4	US-09-362-842-2
23	298	14.2	332	4	US-09-561-763-5
24	298	14.2	332	4	US-09-431-367B-5
25	283.5	13.5	313	3	US-09-336-643A-81
26	283.5	13.5	313	4	US-09-561-763-8
27	283.5	13.5	313	4	US-09-431-367B-8

28	251	11.9	336	1	US-08-332-312-4	Sequence 4, Appli
29	248.5	11.8	401	4	US-09-561-763-11	Sequence 11, Appl
30	248.5	11.8	401	4	US-09-431-367B-11	Sequence 11, Appl
31	246.5	11.7	395	4	US-09-362-842-6	Sequence 6, Appli
32	240	11.4	618	1	US-08-332-312-2	Sequence 2, Appli
33	223.5	10.6	257	4	US-09-949-016-6654	Sequence 6654, Ap
34	223.5	10.6	273	4	US-09-949-016-7794	Sequence 7794, Ap
35	217.5	10.3	730	4	US-09-362-842-4	Sequence 4, Appli
36	217.5	10.3	741	4	US-09-362-842-67	Sequence 67, Appl
37	217.5	10.3	741	4	US-09-270-767-45442	Sequence 45442, A
38	195	9.3	383	3	US-08-749-816-4	Sequence 4, Appli
39	195	9.3	383	3	US-09-144-914-7	Sequence 7, Appli
40	175.5	8.3	107	3	US-09-236-080-4	Sequence 4, Appli
41	154.5	7.3	1153	4	US-09-362-842-8	Sequence 8, Appli
42	148.5	7.1	132	4	US-09-362-842-10	Sequence 10, Appli
43	148.5	7.1	347	3	US-08-749-816-3	Sequence 3, Appli
44	148.5	7.1	347	3	US-09-144-914-6	Sequence 6, Appli
45	124	5.9	646	3	US-09-336-643A-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-144-914-5
; Sequence 5, Application US/09144914
; Patent No. 6309855
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Fink, Michel
; APPLICANT: Lazdunski, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 989.6705CIP
; CURRENT APPLICATION NUMBER: US/09/144,914
; CURRENT FILING DATE: 1998-09-01
; EARLIER APPLICATION NUMBER: 08/749,816
; EARLIER FILING DATE: 1996-11-15
; EARLIER APPLICATION NUMBER: 60/095,234
; EARLIER FILING DATE: 1998-08-04
; EARLIER APPLICATION NUMBER: FR 96/01565
; EARLIER FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Murine
; FEATURE:
; OTHER INFORMATION: TASK
US-09-144-914-5

Query Match	100.0%;	Score 2105;	DB 3;	Length 405;
Best Local Similarity	100.0%;	Pred. No. 1.7e-230;	Mismatches 0;	Gaps 0;
Matches 405;	Conservative 0;			
Qy	1	ENVRTALIVCTFYLLVGA	VFDALESEPMIERQRLERLRLRARNYINSEGGYBELE	60
Db	1	ENVRTALIVCTFYLLVGA	VFDALESEPMIERQRLERLRLRARNYINSEGGYBELE	60
Qy	61	RVVLRLKPKAGVQWR	FAGSFYFAITVITIGYGHAAAPSTDDGGKVFQCFMAYALLGLPLTLI	120
Db	61	RVVLRLKPKAGVQWR	FAGSFYFAITVITIGYGHAAAPSTDDGGKVFQCFMAYALLGLPLTLI	120
Qy	121	MFQSLGRINTFVYLLHRAKRG	IGMBAEVSMMANVLI GFVSCISTLCIGAAAFSYVER	180
Db	121	MFQSLGRINTFVYLLHRAKRG	IGMBAEVSMMANVLI GFVSCISTLCIGAAAFSYVER	180
Qy	181	WTFQAYYCFITTTTIGFGDY	VALQDQALQOTQPVVAFSFVYILTGLTVIGAFNLVV	240
Db	181	WTFQAYYCFITTTTIGFGDY	VALQDQALQOTQPVVAFSFVYILTGLTVIGAFNLVV	240


```
US-09-949-016-7809
; Sequence 7809, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7809
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7809

Query Match      16.2%; Score 341; DB 4; Length 440;
Best Local Similarity 33.2%; Pred. No. 1.1e-29;
Matches 90; Conservative 42; Mismatches 91; Indels 48; Gaps 7;

Qy 6 LALIVCTFTYLLVGAAPVDALESEPE-MIERQRLRLQLRLARYNLSE-----53
Db 54 LALLALVLLVSGALVFRALQEPHQOQRELGEVREKFLRAHPVCVSDQELGLIKEVA 113

Qy 54 ---GGELELRLVLRKPKAGVOMRRFAGSFYFAITVTTTIGYGHAAAPSTDGKVKFCWFY 110
Db 114 DALGGADPEPNTSNTSNSSHA---WDLGSAFFSGTITTTIGYGNVALRTDAGRLFCIFY 170

Qy 111 ALLGIPLTLMFQSLGERINTFVRYLLHRAKRGGLMRHAE-----VSMANMVL 158
Db 171 ALVGIPLFGILLAGVDRGLGSLRH-----GIGHIEAFLKWHVPPPELVRLVSAML 221

Qy 159 IGFVSCISLTCIGAAAFSYRWTFFQAYYCFITLTITIGFDVVALQKQALQTPQYV 218
Db 222 FLIGCLLFLVLTFTFVCYMEDWKLKLAIEYFVITLTITVGGDYVAGADPR--QDSPAYQ 279

Qy 219 AFSFVYLTG-----LTVIGAFNLVLR 242
Db 280 PLVWFVILLGLAYFASVLTITIGNWRVVSRR 310

RESULT 14
US-09-236-080-2
; Sequence 2, Application US/09236080
; Patent No. 6242217
; GENERAL INFORMATION:
; APPLICANT: Helen Meadows
; APPLICANT: Conrad Chapman
; TITLE OF INVENTION: No. 6242217el Compounds
; FILE REFERENCE: GP30031
; CURRENT APPLICATION NUMBER: US/09/236,080
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-080-2

Query Match      16.0%; Score 337; DB 3; Length 411;
Best Local Similarity 29.6%; Pred. No. 2.7e-29;
Matches 86; Conservative 62; Mismatches 101; Indels 42; Gaps 9;

Qy 1 ENVRTLALIVCTFTYLLVGAAPVDALESEPEMIERQRLRLQLRLARYNLSEGGYBELE 60
```

```
Db 45 KTVSTIFLVV--VLYLIIGATVFKALEQHEISQRTTIVIQKTFISQHSVCVNS--TELD 100
Qy 61 RVVRL-KPHKAGV-----QWRPAGSFYFAITVTTTIGYGHAAAPSTDGKVKFCM 108
Db 101 ELIQQIVAAINAGIIPLGNTSNOISHWDLGSSFFAGTIVTTTIGFNGISPRTEGGKIFCI 160
Qy 109 FYALLGIPLTLMFQSLGERI-----NTFVRYLLHRAKRGGLMRHAEVSNMNM 156
Db 161 IYALLGIPLFGLLAGVDQDGLTIFGKIAKVEDTIFKNVSTK-----IRIST 211
Qy 157 VLIQFVSCISLTCIGAAAFSYRWTFFQAYYCFITLTITIGFDVVALQKQALQTPQ 216
Db 212 IIFILFGCVLFVALPAIIFKHIEGWSALDAIYFWITLTITIGFDYVAGSD--IEYLD 269
Qy 217 YVAFSFVYILTGLTVIGAFNLV--VLRPMTMADEKRD-AEHRALLTHN 264
Db 270 YKPVMFWILLVGLAYFAAVLSMIGDMLRVISKTKKEVGEFRAHAAEWNTAN 320

RESULT 15
US-09-336-643A-83
; Sequence 83, Application US/09336643A
; Patent No. 6399761
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. 6399761el Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643A
; CURRENT FILING DATE: 1999-06-18
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 411
; TYPE: PRT
; ORGANISM: H. sapiens
US-09-336-643A-83

Query Match      16.0%; Score 337; DB 3; Length 411;
Best Local Similarity 29.6%; Pred. No. 2.7e-29;
Matches 86; Conservative 62; Mismatches 101; Indels 42; Gaps 9;

Qy 1 ENVRTLALIVCTFTYLLVGAAPVDALESEPEMIERQRLRLQLRLARYNLSEGGYBELE 60
Db 45 KTVSTIFLVV--VLYLIIGATVFKALEQHEISQRTTIVIQKTFISQHSVCVNS--TELD 100
Qy 61 RVVRL-KPHKAGV-----QWRPAGSFYFAITVTTTIGYGHAAAPSTDGKVKFCM 108
Db 101 ELIQQIVAAINAGIIPLGNTSNOISHWDLGSSFFAGTIVTTTIGFNGISPRTEGGKIFCI 160
Qy 109 FYALLGIPLTLMFQSLGERI-----NTFVRYLLHRAKRGGLMRHAEVSNMNM 156
Db 161 IYALLGIPLFGLLAGVDQDGLTIFGKIAKVEDTIFKNVSTK-----IRIST 211
Qy 157 VLIQFVSCISLTCIGAAAFSYRWTFFQAYYCFITLTITIGFDVVALQKQALQTPQ 216
Db 212 IIFILFGCVLFVALPAIIFKHIEGWSALDAIYFWITLTITIGFDYVAGSD--IEYLD 269
Qy 217 YVAFSFVYILTGLTVIGAFNLV--VLRPMTMADEKRD-AEHRALLTHN 264
Db 270 YKPVMFWILLVGLAYFAAVLSMIGDMLRVISKTKKEVGEFRAHAAEWNTAN 320
```

Search completed: September 15, 2005, 22:40:27
Job time : 32 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2005, 22:40:25 ; Search time 169 Seconds
(without alignments)
970.389 Million cell updates/sec

Title: US-09-939-483-5
Perfect score: 2105
Sequence: 1 ENVFTLALIVCTFYLLVGA.....STGLHSLAARGLMKRRSSV 405

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1812044 seqs, 404927589 residues

Total number of hits satisfying chosen parameters: 1812044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

```
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2105	100.0	405	9 US-09-939-484-5	Sequence 5, Appli
2	2105	100.0	405	9 US-09-939-483-5	Sequence 5, Appli
3	2065.5	98.1	412	14 US-10-146-733-9	Sequence 9, Appli
4	1819	86.4	394	9 US-09-939-484-4	Sequence 4, Appli
5	1819	86.4	394	9 US-09-939-483-4	Sequence 4, Appli
6	1819	86.4	394	9 US-09-798-584-15	Sequence 15, Appli
7	1819	86.4	394	14 US-10-146-733-17	Sequence 17, Appli
8	1819	86.4	394	14 US-10-146-733-18	Sequence 18, Appli
9	1819	86.4	394	18 US-10-820-474A-68	Sequence 68, Appli
10	1819	86.4	394	18 US-10-756-149-5724	Sequence 5724, Ap
11	1819	86.4	395	14 US-10-146-733-8	Sequence 8, Appli

12	1392.5	66.2	312	8 US-08-816-011-55	Sequence 55, Appli
13	1392.5	66.2	312	17 US-10-870-492-55	Sequence 55, Appli
14	1306	62.0	258	9 US-09-746-491-61	Sequence 61, Appli
15	1200	57.0	233	15 US-10-459-190-15	Sequence 15, Appli
16	1100	52.3	374	9 US-09-798-584-1	Sequence 1, Appli
17	1100	52.3	374	14 US-10-146-733-41	Sequence 41, Appli
18	1100	52.3	374	15 US-10-257-022-6	Sequence 6, Appli
19	1100	52.3	374	15 US-10-074-978A-194	Sequence 194, App
20	1079.5	51.3	387	15 US-10-074-978A-195	Sequence 195, App
21	1062.5	50.5	365	9 US-09-746-491-60	Sequence 60, Appli
22	836.5	39.7	330	9 US-09-746-491-59	Sequence 59, Appli
23	836.5	39.7	330	15 US-10-173-999-42	Sequence 42, Appli
24	836.5	39.7	330	15 US-10-074-978A-192	Sequence 192, App
25	836.5	39.7	330	15 US-10-146-733-5	Sequence 5, Appli
26	828.5	39.4	330	9 US-09-746-491-58	Sequence 58, Appli
27	828.5	39.4	330	15 US-10-074-978A-191	Sequence 191, App
28	828.5	39.4	330	15 US-10-336-472-76	Sequence 76, Appli
29	828.5	39.4	330	9 US-09-746-491-22	Sequence 22, Appli
30	828.5	39.4	330	14 US-10-146-733-2	Sequence 2, Appli
31	828.5	39.4	400	15 US-10-257-022-13	Sequence 13, Appli
32	828.5	39.4	400	15 US-10-450-763-59632	Sequence 59632, A
33	779.5	37.0	436	18 US-09-864-761-34389	Sequence 34389, A
34	768	36.5	279	9 US-10-074-978A-24	Sequence 24, Appli
35	610	29.0	212	15 US-10-424-599-216417	Sequence 216417, A
36	518	24.6	179	15 US-10-451-892-10	Sequence 10, Appli
37	364.5	17.3	292	15 US-09-852-386-74	Sequence 129, App
38	362.5	17.2	534	10 US-10-461-862-129	Sequence 6, Appli
39	362	17.2	487	17 US-10-451-892-6	Sequence 4, Appli
40	359	17.1	292	15 US-10-459-190-4	Sequence 8, Appli
41	359	17.1	292	15 US-10-343-903-8	Sequence 132, App
42	357.5	17.0	295	16 US-10-461-862-132	Sequence 2, Appli
43	356.5	16.9	406	17 US-10-121-966-2	Sequence 2, Appli
44	355	16.9	294	13 US-10-451-892-2	Sequence 2, Appli
45	355	16.9	294	15 US-10-451-892-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-939-484-5
; Sequence 5, Application US/09939484
; Patent No. US20020032322A1
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Fink, Michel
; APPLICANT: Lardunski, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 1201-CIP-DIV-00
; CURRENT APPLICATION NUMBER: US/09/939,484
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/144,914
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 08/749,816
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: 60/095,234
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: FR 96/01565
; PRIOR FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Murine
; FEATURE:
; OTHER INFORMATION: TASK
US-09-939-484-5

Query Match 100.0%; Score 2105; DB 9; Length 405;
Best Local Similarity 100.0%; Pred. No. 2.1e-198;

Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENVRTALIVCTFTYLLVGAAVFDALSEPEMIERQRLERQLELRARYNLSEGGYELE 60
Db 1 ENVRTALIVCTFTYLLVGAAVFDALSEPEMIERQRLERQLELRARYNLSEGGYELE 60

Qy 61 RVVLRPKHKGAVQWRFAGSFYFAITVTTTIGYGHAAAPSTDGKVFQCMFYALLGIPLTLI 120
Db 61 RVVLRPKHKGAVQWRFAGSFYFAITVTTTIGYGHAAAPSTDGKVFQCMFYALLGIPLTLI 120

Qy 121 MFQSLGERINTFVRYLLHRAKRGLMRHAESVSMANMVLIGFVSCISTLCIGAAAFSYER 180
Db 121 MFQSLGERINTFVRYLLHRAKRGLMRHAESVSMANMVLIGFVSCISTLCIGAAAFSYER 180

Qy 181 WTFQAYYVCITLTTIGFGDYVALQDQALQTOPOQYVAFSFVYILTGLTVIGAFNLV 240
Db 181 WTFQAYYVCITLTTIGFGDYVALQDQALQTOPOQYVAFSFVYILTGLTVIGAFNLV 240

Qy 241 LRFMTMAEDKRDRAEHRALLTHNGQAVGLGGLSCLSGSLGDRVPRDPVTCAAAAGGVG 300
Db 241 LRFMTMAEDKRDRAEHRALLTHNGQAVGLGGLSCLSGSLGDRVPRDPVTCAAAAGGVG 300

Qy 301 GVGSGRNVYAELHFGSMCSCLYWKSREKLOYSIPIIIPDLSTSDTCVEHSHSPGG 360
Db 301 GVGSGRNVYAELHFGSMCSCLYWKSREKLOYSIPIIIPDLSTSDTCVEHSHSPGG 360

Qy 361 GGRYSDTPSPHCLCSGTORSATSSVSTGLHSLAAFRGLMKRRSSV 405
Db 361 GGRYSDTPSPHCLCSGTORSATSSVSTGLHSLAAFRGLMKRRSSV 405

RESULT 2

US-09-939-483-5
; Sequence 5, Application US/09939483
; Patent No. US2002094558A1
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Fink, Michel
; APPLICANT: Lazdunski, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 1201-CIP-DIV-2-00
; CURRENT APPLICATION NUMBER: US/09/939,483
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/144,914
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 08/749,816
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: 60/095,234
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: FR 96/01565
; PRIOR FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Murine
; FEATURE:
; OTHER INFORMATION: TASK
US-09-939-483-5

Query Match 100.0%; Score 2105; DB 9; Length 405;
Best Local Similarity 100.0%; Pred. No. 2.1e-198;
Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENVRTALIVCTFTYLLVGAAVFDALSEPEMIERQRLERQLELRARYNLSEGGYELE 60
Db 1 ENVRTALIVCTFTYLLVGAAVFDALSEPEMIERQRLERQLELRARYNLSEGGYELE 60

Qy 61 RVVLRPKHKGAVQWRFAGSFYFAITVTTTIGYGHAAAPSTDGKVFQCMFYALLGIPLTLI 120
Db 61 RVVLRPKHKGAVQWRFAGSFYFAITVTTTIGYGHAAAPSTDGKVFQCMFYALLGIPLTLI 120

Db 61 RVVLRPKHKGAVQWRFAGSFYFAITVTTTIGYGHAAAPSTDGKVFQCMFYALLGIPLTLI 120

Qy 121 MFQSLGERINTFVRYLLHRAKRGLMRHAESVSMANMVLIGFVSCISTLCIGAAAFSYER 180
Db 121 MFQSLGERINTFVRYLLHRAKRGLMRHAESVSMANMVLIGFVSCISTLCIGAAAFSYER 180

Qy 181 WTFQAYYVCITLTTIGFGDYVALQDQALQTOPOQYVAFSFVYILTGLTVIGAFNLV 240
Db 181 WTFQAYYVCITLTTIGFGDYVALQDQALQTOPOQYVAFSFVYILTGLTVIGAFNLV 240

Qy 241 LRFMTMAEDKRDRAEHRALLTHNGQAVGLGGLSCLSGSLGDRVPRDPVTCAAAAGGVG 300
Db 241 LRFMTMAEDKRDRAEHRALLTHNGQAVGLGGLSCLSGSLGDRVPRDPVTCAAAAGGVG 300

Qy 301 GVGSGRNVYAELHFGSMCSCLYWKSREKLOYSIPIIIPDLSTSDTCVEHSHSPGG 360
Db 301 GVGSGRNVYAELHFGSMCSCLYWKSREKLOYSIPIIIPDLSTSDTCVEHSHSPGG 360

Qy 361 GGRYSDTPSPHCLCSGTORSATSSVSTGLHSLAAFRGLMKRRSSV 405
Db 361 GGRYSDTPSPHCLCSGTORSATSSVSTGLHSLAAFRGLMKRRSSV 405

RESULT 3

US-10-146-733-9
; Sequence 9, Application US/10146733
; Publication No. US20030165891A1
; GENERAL INFORMATION:
; APPLICANT: Curtiss, Rory A.J.
; APPLICANT: Glucksmann, Maria A.
; TITLE OF INVENTION: NOVEL TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615,
; TITLE OF INVENTION: HNMDA-1, TWIK-9, alpha2delta-4, 54414, AND 53763 MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: MNI-248
; CURRENT APPLICATION NUMBER: US/10/146,733
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/185,938
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 09/515,520
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 09/518,866
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: US 60/195,734
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US 60/195,993
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: US 60/199,799
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: US 60/233,537
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: US 60/235,018
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 60/235,059
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 60/256,240
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/256,588
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/258,028
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: US 09/796,720
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/828,035
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 09/833,081
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 09/843,128
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/957,683
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: US 09/964,252
; PRIOR FILING DATE: 2001-09-25

```
; PRIOR APPLICATION NUMBER: US 09/964,256
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 10/024,623
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-146-733-9

Query Match      98.1%; Score 2065.5; DB 14; Length 412;
Best Local Similarity 98.0%; Pred. No. 1.7e-194;
Matches 400; Conservative 3; Mismatches 2; Indels 3; Gaps 2;

Qy 1 ENVRTLALIVCTFTYLLVGAADFDALESEPEMIERQRLERLQLELRARYNLSEGGYELE 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5 QNVRTLALIVCTFTYLLVGAADFDALESEPEMIERQRLERLQLELRARYNLSEGGYELE 64

Qy 61 RVVRLKPKHAGVQWRFGAGSFYFAITVTTTIGYGHAAAPSTDGKVFVCMFYALLGIPLTLI 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
65 RVVRLKPKHAGVQWRFGAGSFYFAITVTTTIGYGHAAAPSTDGKVFVCMFYALLGIPLTIV 124

Qy 121 MFQSLGERINTFVRYLLHRAKRGIMRHAESVMANMVLIGFVSCISTICIGAAAFSYVER 180
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
125 MFQSLGERINTFVRYLLHRAKRGIMRHAESVMANMVLIGFVSCISTICIGAAAFSYVER 184

Qy 181 WFFQAYYYCFITLTTIGFDYVALQDQALQTPQYVAFSFVYLTGLTVIGAFNLVW 240
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
185 WFFQAYYYCFITLTTIGFDYVALQDQALQTPQYVAFSFVYLTGLTVIGAFNLVW 244

Qy 241 LRFTMTNAEDEKRAEHRALLTHNQAGGLGCLSGSLGDPVPRDPVTCAAAAG--G 297
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
245 LRFTMTNAEDEKRAEHRALLTHNQAGGLGCLSGSLGDPVPRDPVTCAAAAGGMG 304

Qy 298 VGVGGSGFRNVYAEVLHFQSMCCLWYKREKLOYSIPIIPDLSTSDTCVEHSHSS 357
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
305 VGVGGSGFRNVYAEVLHFQSMCCLWYKREKLOYSIPIIPDLSTSDTCVEHSHSS 364

Qy 358 PGGGRYSDTSPHCLCGTQRSATSSVSTGLHSLAFAFRGLMKRRSSV 405
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
365 PGGGRYSDTSPHCLCGTQRSATSSVSTGLHSLATFRGLMKRRSSV 412

RESULT 4
US-09-939-484-4
; Sequence 4, Application US/09939484
; Patent No. US2002003232A1
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Fink, Michel
; APPLICANT: Lazdunski, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 1201-CIP-DIV-00
; CURRENT APPLICATION NUMBER: US/09/939,484
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/144,914
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 08/749,816
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: 60/095,234
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: FR 96/01565
; PRIOR FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match      86.4%; Score 1819; DB 9; Length 394;
Best Local Similarity 88.1%; Pred. No. 3.1e-170;
Matches 357; Conservative 9; Mismatches 25; Indels 14; Gaps 2;

; FEATURE:
; OTHER INFORMATION: TASK
US-09-939-484-4

Query Match      86.4%; Score 1819; DB 9; Length 394;
Best Local Similarity 88.1%; Pred. No. 3.1e-170;
Matches 357; Conservative 9; Mismatches 25; Indels 14; Gaps 2;

Qy 1 ENVRTLALIVCTFTYLLVGAADFDALESEPEMIERQRLERLQLELRARYNLSEGGYELE 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4 QNVRTLALIVCTFTYLLVGAADFDALESEPEMIERQRLERLQLELRARYNLSEGGYELE 63

Qy 61 RVVRLKPKHAGVQWRFGAGSFYFAITVTTTIGYGHAAAPSTDGKVFVCMFYALLGIPLTLI 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
64 RVVRLKPKHAGVQWRFGAGSFYFAITVTTTIGYGHAAAPSTDGKVFVCMFYALLGIPLTIV 123

Qy 121 MFQSLGERINTFVRYLLHRAKRGIMRHAESVMANMVLIGFVSCISTICIGAAAFSYVER 180
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
124 MFQSLGERINTFVRYLLHRAKRGIMRHAESVMANMVLIGFVSCISTICIGAAAFSHYEH 183

Qy 181 WFFQAYYYCFITLTTIGFDYVALQDQALQTPQYVAFSFVYLTGLTVIGAFNLVW 240
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
184 WFFQAYYYCFITLTTIGFDYVALQDQALQTPQYVAFSFVYLTGLTVIGAFNLVW 243

Qy 241 LRFTMTNAEDEKRAEHRALLTHNQAGGLGCLSGSLGDPVPRDPVTCAAAAGGVV 300
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
244 LRFTMTNAEDEKRAEHRALLTRNQAGGGG-----GGSAHTTDTASAAAA----- 291

Qy 301 GVGSGFRNVYAEVLHFQSMCCLWYKREKLOYSIPIIPDLSTSDTCVEHSHSSPGG 360
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
292 --GGGGRNVYAEVLHFQSMCCLWYKREKLOYSIPIIPDLSTSDTCVEHSHSSPGG 349

Qy 361 GGRYSDTSPHCLCGTQRSATSSVSTGLHSLAFAFRGLMKRRSSV 405
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
350 GGRYSDTSPHCLCGTQRSATSSVSTGLHSLSTFRGLMKRRSSV 394

RESULT 5
US-09-939-483-4
; Sequence 4, Application US/09939483
; Patent No. US20020094558A1
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Fink, Michel
; APPLICANT: Lazdunski, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 1201-CIP-DIV-2-00
; CURRENT APPLICATION NUMBER: US/09/939,483
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/144,914
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 08/749,816
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: 60/095,234
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: FR 96/01565
; PRIOR FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens

; FEATURE:
; OTHER INFORMATION: TASK
US-09-939-483-4

Query Match      86.4%; Score 1819; DB 9; Length 394;
Best Local Similarity 88.1%; Pred. No. 3.1e-170;
Matches 357; Conservative 9; Mismatches 25; Indels 14; Gaps 2;
```

```
Qy 1 ENVRTLALIVCTFTYLLVGAADFALSEPEMIERQRLRQLRRLRYNLSQGGYEEL 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4 QNVRTLALIVCTFTYLLVGAADFALSEPELIERQRLRQLRRLRYNLSQGGYEEL 63

Qy 61 RVVRLKPKHAGVQWRFAGSFYFAITVTITIGYGHAAAPSTDGKVKFCMFVALLGIPLT 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
64 RVVRLKPKHAGVQWRFAGSFYFAITVTITIGYGHAAAPSTDGKVKFCMFVALLGIPLT 123

Qy 121 MFQSLGERINTFVRYLLHRAKGLGMRHAEVSMANMVLIGFVSCISTLCIGAAAFSYYER 180
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
124 MFQSLGERINTFVRYLLHRAKGLGMRHADVSMANMVLIGFVSCISTLCIGAAAFSYYEH 183

Qy 181 WTFQAYYVCFITLTITIGFDYVALQDQALQTOQYVAFSVYILTGLTVIGAFNLVV 240
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
184 WTFQAYYVCFITLTITIGFDYVALQDQALQTOQYVAFSVYILTGLTVIGAFNLVV 243

Qy 241 LRFTMNAEDKRDRAEHRALLTHNGQAVGLGSLCCLSGSLGDVVRPDPVTCAAAGGVG 300
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
244 LRFTMNAEDKRDRAEHRALLTRNGQAGGGG-----GGSAAHTTDTASSTAAA----- 291

Qy 301 GVGSGFRNVYAEVLHFQSMCCLWYKSREKLOYSIPIPRDLSTSDTCVEHSHSPGG 360
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
292 --GGGFRNVYAEVLHFQSMCCLWYKSREKLOYSIPIPRDLSTSDTCVEHSHSPGG 349

Qy 361 GGRYSDTPSPHCLCSGTQRSATSSVSTGLHSLAAPRGLMKRRSSV 405
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
350 GGRYSDTPSRCLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394
```

RESULT 6

```
US-09-798-584-15
; Sequence 15, Application US/09798584
; Patent No. US20020102676A1
; GENERAL INFORMATION:
; APPLICANT: Mu, David
; APPLICANT: Powers, Scott
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: KCNB: A No. US20020102676A1el Potassium Channel Protein
; FILE REFERENCE: 018781-004010US
; CURRENT APPLICATION NUMBER: US/09/798,584
; CURRENT FILING DATE: 2001-03-03
; PRIOR APPLICATION NUMBER: US 60/186,951
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human potassium channel KCNK3 (TASK1)
US-09-798-584-15
```

```
Query Match 86.4%; Score 1819; DB 9; Length 394;
Best Local Similarity 88.1%; Pred. No. 3.1e-170;
Matches 357; Conservative 9; Mismatches 25; Indels 14; Gaps 2;
```

```
Qy 1 ENVRTLALIVCTFTYLLVGAADFALSEPEMIERQRLRQLRRLRYNLSQGGYEEL 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4 QNVRTLALIVCTFTYLLVGAADFALSEPELIERQRLRQLRRLRYNLSQGGYEEL 63

Qy 61 RVVRLKPKHAGVQWRFAGSFYFAITVTITIGYGHAAAPSTDGKVKFCMFVALLGIPLT 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
64 RVVRLKPKHAGVQWRFAGSFYFAITVTITIGYGHAAAPSTDGKVKFCMFVALLGIPLT 123

Qy 121 MFQSLGERINTFVRYLLHRAKGLGMRHAEVSMANMVLIGFVSCISTLCIGAAAFSYYER 180
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
124 MFQSLGERINTFVRYLLHRAKGLGMRHADVSMANMVLIGFVSCISTLCIGAAAFSYYEH 183

Qy 181 WTFQAYYVCFITLTITIGFDYVALQDQALQTOQYVAFSVYILTGLTVIGAFNLVV 240
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
184 WTFQAYYVCFITLTITIGFDYVALQDQALQTOQYVAFSVYILTGLTVIGAFNLVV 243
```

```
Qy 241 LRFTMNAEDKRDRAEHRALLTHNGQAVGLGSLCCLSGSLGDVVRPDPVTCAAAGGVG 300
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
244 LRFTMNAEDKRDRAEHRALLTRNGQAGGGG-----GGSAAHTTDTASSTAAA----- 291

Qy 301 GVGSGFRNVYAEVLHFQSMCCLWYKSREKLOYSIPIPRDLSTSDTCVEHSHSPGG 360
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
292 --GGGFRNVYAEVLHFQSMCCLWYKSREKLOYSIPIPRDLSTSDTCVEHSHSPGG 349

Qy 361 GGRYSDTPSPHCLCSGTQRSATSSVSTGLHSLAAPRGLMKRRSSV 405
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
350 GGRYSDTPSRCLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394
```

RESULT 7

```
US-10-146-733-17
; Sequence 17, Application US/10146733
; Publication No. US20030165891A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: NOVEL TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615,
; TITLE OF INVENTION: HNDA-1, TWIK-9, alpha2delta-4, 54414, AND 53763 MOLSCULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: MNI-248
; CURRENT APPLICATION NUMBER: US/10/146,733
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/185,938
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 09/515,520
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 09/518,866
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: US 60/195,734
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US 60/195,993
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: US 60/199,799
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: US 60/233,537
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: US 60/235,018
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 60/235,059
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 60/256,240
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/256,588
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/258,028
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: US 09/796,720
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/828,035
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 09/833,081
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 09/843,128
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/957,683
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: US 09/964,252
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 09/964,256
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 10/024,623
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
```



```
US-10-146-733-17
Query Match      86.4%; Score 1819; DB 14; Length 394;
Best Local Similarity 88.1%; Pred. No. 3.1e-170;
Matches 357; Conservative 9; Mismatches 25; Indels 14; Gaps 2;

Qy 1 ENVRTALIVCTFTYLLVGAAPDVALESEPEMIERQLELRQLELRARYNLSEGGYELE 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4 QNVRTALIVCTFTYLLVGAAPDVALESEPELIERQLELRQLELRARYNLSEGGYELE 63
Qy 61 RVVLRLKPKHAGVQWRPAGSFYFALTITVITIGYGHAAAPSTDGKVFQVCFMFIALLGPIPLTL 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
64 RVVLRLKPKHAGVQWRPAGSFYFALTITVITIGYGHAAAPSTDGKVFQVCFMFIALLGPIPLTLV 123
Qy 121 MFQSLGERINTFVRYLLHRAKGLGMRHAESVMANVILGFVSCISTLCIGAAAFSYHYER 180
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
124 MFQSLGERINTLVRYLLHRAKGLGMRADYSVMANVILGFSCISTLCIGAAAFSHYEH 183
Qy 181 WTFQAYYYCFITLTITIGFDYVALQDQALQTOQVYAFSFVYLLTGLTVIGAFNLV 240
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
184 WTFQAYYYCFITLTITIGFDYVALQDQALQTOQVYAFSFVYLLTGLTVIGAFNLV 243
Qy 241 LRFMTMAEDEKRDHAERHALLTHNGQAVLGGLSCLSGSLGSDVRPRDPTVTCAAAAGGVGV 300
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
244 LRFMTMAEDEKRDHAERHALLTRNGQAGGGG-----GSAHTTDTASSTAAA----- 291
Qy 301 GVGSGFRNVYAEVLHFQSMCCLWYKREKLYQSIPIPRDLSTSDTCVEHSHSPGG 360
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
292 --GGGFRNVYAEVLHFQSMCCLWYKREKLYQSIPIPRDLSTSDTCVEQSHSPGG 349
Qy 361 GGRYSDTPSHPCLCSGTORSATSSVSTGLHSLAARFGLMKRRSSV 405
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
350 GGRYSDTPSRRLCCLSGAPRSATSSVSTGLHSLSTRFGLMKRRSSV 394

RESULT 8
US-10-146-733-18
; Sequence 18, Application US/10146733
; Publication No. US20030165891A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Roly A.J.
; APPLICANT: Gluckmann, Maria A.
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: NOVEL TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615,
; TITLE OF INVENTION: HMMDA-1, TWIK-9, alpha2delta-4, 54414, AND 53763 MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: MNI-248
; CURRENT APPLICATION NUMBER: US/10/146,733
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/185,938
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 09/515,520
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 09/518,866
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: US 60/195,734
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US 60/195,993
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: US 60/199,799
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: US 60/233,537
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: US 60/235,018
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 60/235,059
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 60/256,240
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/256,588
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/258,028
; PRIOR FILING DATE: 2000-12-21

Query Match      86.4%; Score 1819; DB 14; Length 394;
Best Local Similarity 88.1%; Pred. No. 3.1e-170;
Matches 357; Conservative 9; Mismatches 25; Indels 14; Gaps 2;

Qy 1 ENVRTALIVCTFTYLLVGAAPDVALESEPEMIERQLELRQLELRARYNLSEGGYELE 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4 QNVRTALIVCTFTYLLVGAAPDVALESEPELIERQLELRQLELRARYNLSEGGYELE 63
Qy 61 RVVLRLKPKHAGVQWRPAGSFYFALTITVITIGYGHAAAPSTDGKVFQVCFMFIALLGPIPLTL 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
64 RVVLRLKPKHAGVQWRPAGSFYFALTITVITIGYGHAAAPSTDGKVFQVCFMFIALLGPIPLTLV 123
Qy 121 MFQSLGERINTFVRYLLHRAKGLGMRHAESVMANVILGFVSCISTLCIGAAAFSYHYER 180
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
124 MFQSLGERINTLVRYLLHRAKGLGMRADYSVMANVILGFSCISTLCIGAAAFSHYEH 183
Qy 181 WTFQAYYYCFITLTITIGFDYVALQDQALQTOQVYAFSFVYLLTGLTVIGAFNLV 240
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
184 WTFQAYYYCFITLTITIGFDYVALQDQALQTOQVYAFSFVYLLTGLTVIGAFNLV 243
Qy 241 LRFMTMAEDEKRDHAERHALLTHNGQAVLGGLSCLSGSLGSDVRPRDPTVTCAAAAGGVGV 300
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
244 LRFMTMAEDEKRDHAERHALLTRNGQAGGGG-----GSAHTTDTASSTAAA----- 291
Qy 301 GVGSGFRNVYAEVLHFQSMCCLWYKREKLYQSIPIPRDLSTSDTCVEHSHSPGG 360
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
292 --GGGFRNVYAEVLHFQSMCCLWYKREKLYQSIPIPRDLSTSDTCVEQSHSPGG 349
Qy 361 GGRYSDTPSHPCLCSGTORSATSSVSTGLHSLAARFGLMKRRSSV 405
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
350 GGRYSDTPSRRLCCLSGAPRSATSSVSTGLHSLSTRFGLMKRRSSV 394
```

```
; APPLICANT: HILLMAN, JENNIFER L.
; APPLICANT: BANDMAN, OLGA
; TITLE OF INVENTION: SIGNAL PEPTIDE-CONTAINING MOLECULES
; FILE REFERENCE: 039386-1568
; CURRENT APPLICATION NUMBER: US/10/820,474A
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: 09/720,533
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: PCT/US99/14484
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/090,762
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/094,983
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: 60/102,686
; PRIOR FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 68
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte Clone No: 1229438
US-10-820-474A-68

Query Match      86.4%; Score 1819; DB 18; Length 394;
Best Local Similarity 88.1%; Pred. No. 3.1e-170;
Matches 357; Conservative 9; Mismatches 25; Indels 14; Gaps 2;

Qy 1 ENVRTLALIVCTFTYLLVGAAVFDALSEPEMIERQRLRLQLELRARYNLSGGYEELE 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4 QNVRTLALIVCTFTYLLVGAAVFDALSEPELIERQRLRLQLELRARYNLSQGYEELE 63
Qy 61 RVVRLKPKHKGAVQWRPAGSFYFAITVTTTIGYGHAAAPSTDGKVFQVCFMVFALLGIPLTLI 120
Db 64 RVVRLKPKHKGAVQWRPAGSFYFAITVTTTIGYGHAAAPSTDGKVFQVCFMVFALLGIPLTIV 123
Qy 121 MFQSLGERINTFVRYLLHRAKGLGMRHAESVMANMVLIGFVSCISTLCIGAAAFSYER 180
Db 124 MFQSLGERINTFVRYLLHRAKGLGMRRAVDSMANMVLIGFFSCISTLCIGAAAFSHYEH 183
Qy 181 WTFQAYYYCFITLTITGFDGYVALQDQALQTOPOQYVAFSFVYILTGLTVIGAFNLV 240
Db 184 WTFQAYYYCFITLTITGFDGYVALQDQALQTOPOQYVAFSFVYILTGLTVIGAFNLV 243
Qy 241 LRFMTMAEDKRAEHRALLTHNGQAVGLGGLSCLSGSLGDRVPRDPVTCAAAAGGVV 300
Db 244 LRFMTMAEDKRAEHRALLTRNGQAGGGG-----GSAHTTDTASSTAAA----- 291
Qy 301 GVGGGFRNVYAEVLHFQSMCCLWYKREKLOYSIPIPIPRDLSTSDTCVEHSHSPGG 360
Db 292 --GGGFRNVYAEVLHFQSMCCLWYKREKLOYSIPIPIPRDLSTSDTCVEHSHSPGG 349
Qy 361 GGRYSPTPSHPCICSGTQORSALSISSVSTGLHSLAAPRGLMKRRSSV 405
Db 292 --GGGFRNVYAEVLHFQSMCCLWYKREKLOYSIPIPIPRDLSTSDTCVEHSHSPGG 349

RESULT 10
US-10-756-149-5724
; Sequence 5724, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
```

```
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 5724
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-756-149-5724

Query Match      86.4%; Score 1819; DB 18; Length 394;
Best Local Similarity 88.1%; Pred. No. 3.1e-170;
Matches 357; Conservative 9; Mismatches 25; Indels 14; Gaps 2;

Qy 1 ENVRTLALIVCTFTYLLVGAAVFDALSEPEMIERQRLRLQLELRARYNLSGGYEELE 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4 QNVRTLALIVCTFTYLLVGAAVFDALSEPELIERQRLRLQLELRARYNLSQGYEELE 63
Qy 61 RVVRLKPKHKGAVQWRPAGSFYFAITVTTTIGYGHAAAPSTDGKVFQVCFMVFALLGIPLTLI 120
Db 64 RVVRLKPKHKGAVQWRPAGSFYFAITVTTTIGYGHAAAPSTDGKVFQVCFMVFALLGIPLTIV 123
Qy 121 MFQSLGERINTFVRYLLHRAKGLGMRHAESVMANMVLIGFVSCISTLCIGAAAFSYER 180
Db 124 MFQSLGERINTFVRYLLHRAKGLGMRRAVDSMANMVLIGFFSCISTLCIGAAAFSHYEH 183
Qy 181 WTFQAYYYCFITLTITGFDGYVALQDQALQTOPOQYVAFSFVYILTGLTVIGAFNLV 240
Db 184 WTFQAYYYCFITLTITGFDGYVALQDQALQTOPOQYVAFSFVYILTGLTVIGAFNLV 243
Qy 241 LRFMTMAEDKRAEHRALLTHNGQAVGLGGLSCLSGSLGDRVPRDPVTCAAAAGGVV 300
Db 244 LRFMTMAEDKRAEHRALLTRNGQAGGGG-----GSAHTTDTASSTAAA----- 291
Qy 301 GVGGGFRNVYAEVLHFQSMCCLWYKREKLOYSIPIPIPRDLSTSDTCVEHSHSPGG 360
Db 292 --GGGFRNVYAEVLHFQSMCCLWYKREKLOYSIPIPIPRDLSTSDTCVEHSHSPGG 349
Qy 361 GGRYSPTPSHPCICSGTQORSALSISSVSTGLHSLAAPRGLMKRRSSV 405
Db 350 GGRYSPTPSRCLCSGAPRSALSISSVSTGLHSLSTRFGLMKRRSSV 394

RESULT 11
US-10-146-733-8
; Sequence 8, Application US/10146733
; Publication No. US20030165891A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: NOVEL TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615,
; TITLE OF INVENTION: HNMDA-1, TWIK-9, alpha2delta-4, 54414, AND 53763 MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: MNI-248
; CURRENT APPLICATION NUMBER: US/10/146,733
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/185,938
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 09/515,520
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 09/518,866
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: US 60/195,734
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US 60/195,993
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: US 60/199,799
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: US 60/233,537
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: US 60/235,018
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 60/235,059
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 60/256,240
```

```
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/256,588
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/258,028
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: US 09/796,720
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/828,035
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 09/833,081
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 09/843,128
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/957,683
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: US 09/964,252
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 09/964,256
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 10/024,623
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-733-8

Query Match      86.4%; Score 1819; DB 14; Length 395;
Best Local Similarity 88.1%; Pred. No. 3.1e-170; Indels 14; Gaps 2;
Matches 357; Conservative 9; Mismatches 25;

Qy 1 ENVRTALIVCTFTYLLVGAADFALSEPEMIERQRLERLQELRARNYLNSEGYYEEL 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5 QNVRTALIVCTFTYLLVGAADFALSEPELIERQRLERLQELRARNYLNSEGYYEEL 64
Qy 61 RVVRLKPKHAGVQWRPAGSFYFAITVTTTIGYGHAAAPSTDGKVFQVCFMAYALLG 120
Db 65 RVVRLKPKHAGVQWRPAGSFYFAITVTTTIGYGHAAAPSTDGKVFQVCFMAYALLG 124
Qy 121 MFQSLGERINTFVRYLLHRAKGLGMRHAESVMANNVLIQVSCISTICIGAAAFS 180
Db 125 MFQSLGERINTFVRYLLHRAKGLGMRHADVSVMANNVLIQVSCISTICIGAAAFS 184
Qy 181 WTTFFQAYYYCFITLTITIGFDYVALQKQALQTPQYVAFSFYVILTGLTVIGAF 240
Db 185 WTTFFQAYYYCFITLTITIGFDYVALQKQALQTPQYVAFSFYVILTGLTVIGAF 244
Qy 241 LRFMTNNAEDEKRDHRAHLLTHNGQAVGLGSLCGLSGLDGVRPRDPVTCAAAAG 300
Db 245 LRFMTNNAEDEKRDHRAHLLTRNGQAGGGG-----GSAHTTDTASSTAAA 292
Qy 301 GVGSGFRNVYAEVLHFMSCSLMYKREKLOYSIPIMLIPDLSTSDTCVEHSHSP 360
Db 293 --GGGGRNVYAEVLHFMSCSLMYKREKLOYSIPIMLIPDLSTSDTCVEHSHSP 350
Qy 361 GGRYSDTPSHPCLSGTSORSAISSYSTGLHSLAFAFGLMKRRSSV 405
Db 351 GGRYSDTPSHPCLSGTSORSAISSYSTGLHSLAFAFGLMKRRSSV 395

RESULT 12
US-08-816-011-55
; Sequence 55, Application US/08816011
; Publication No. US20030165806A1
; GENERAL INFORMATION:
; APPLICANT: Price, Laura A.
; APPLICANT: Pausch, Mark H.
; TITLE OF INVENTION: Potassium Channels, Nucleotide Sequences
; FILE OF INVENTION: AND METHODS OF USING SAME
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US/09/503,849
; PRIOR FILING DATE: 2000-02-15
; CORRESPONDENCE ADDRESS:

; ADDRESS: American Home Products Corporation
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,011
; FILING DATE: 11-MAR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthews, Gale F.
; REGISTRATION NUMBER: 32,269
; REFERENCE/DOCKET NUMBER: 32,421-C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-683-2134
; TELEFAX: 201-683-4117
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-816-011-55

Query Match      66.2%; Score 1392.5; DB 8; Length 312;
Best Local Similarity 93.0%; Pred. No. 2.4e-128; Indels 9; Gaps 4;
Matches 280; Conservative 2; Mismatches 10;

Qy 1 ENVRTALIVCTFTYLLVGAADFALSEPEMIERQRLERLQELRARNYLNSEGYYEEL 60
Db 13 ENVRTALIVCTFTYLLVGAADFALSEPEMIERQRLERLQELRARNYLNSEGYYEEL 72
Qy 61 RVVRLKPKHAGVQWRPAGSFYFAITVTTTIGYGHAAAPSTDGKVFQVCFMAYALLG 117
Db 73 RVVRLKPKHAGVQWRPAGSFYFAITVTTTIGYGHAAAPSTDGKVFQVCFMAYALLG 132
Qy 118 TLINFQSLGERINTFVRYLLHRAKGLGMRHAESVMANNVLIQVSCISTICIGAAAFS 177
Db 133 TLNVFQSLGERINTFVRYLLHRAKGLGMRHAESVMANNVLIQVSCISTICIGAAAFS 192
Qy 178 YERWTFQAYYYCFITLTITIGFDYVALQKQALQTPQYVAFSFYVILTGLTVIG 235
Db 193 YERWTFQAYYYCFITLTITIGFDYVALQKQALQTPQYVAFS---SCTSSRAHGHRRF 249
Qy 236 LNVVLRPMTNNAEDEKRDHRAHLLTHNGQAVGLGSLCGLSGLDGVRPRDPVTC 294
Db 250 LNVVLRPMTNNAEDEKRDHRAHLLTHNGQAVGLGSLCGLSGLDGVRPRDPVTC 309
Qy 295 A 295
Db 310 A 310

RESULT 13
US-10-870-492-55
; Sequence 55, Application US/10870492
; Publication No. US20050032165A1
; GENERAL INFORMATION:
; APPLICANT: PAUSCH, MARK H.
; TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
; FILE OF INVENTION: AND METHODS OF USING SAME
; FILE REFERENCE: 01142.0114 SEQUENCE LISTING
; CURRENT APPLICATION NUMBER: US/10/870,492
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US/09/503,849
; PRIOR FILING DATE: 2000-02-15
; CORRESPONDENCE ADDRESS:
; APPLICATION NUMBER: 08/816,011
```

```
; PRIOR FILING DATE: 1997-03-11
; PRIOR APPLICATION NUMBER: PCT/US95/14364
; PRIOR FILING DATE: 1995-10-25
; PRIOR APPLICATION NUMBER: 07/332,312
; PRIOR FILING DATE: 1994-10-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 55
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-870-492-55

Query Match
Best Local Similarity 93.0%; Score 1392.5; DB 17; Length 312;
Matches 280; Conservative 2; Mismatches 10; Indels 9; Gaps 4;

Qy 1 ENVTALIVCTFTYLLVGAAVFDALSEPEMIERQRLRLQLELRARYNLSEGGYEELE 60
Db :|||||
Qy 13 ENVTALIVCTFTYLLVGAAVFDALSEPEMIERQRLRLQLELRARYNLSEGGYEELE 72
Db :|||||
Qy 61 RVLRRLPKHKGAVQWRAGSFYFAITVTTTIGYGHAAAPSTDGKV---FCMFYALLGIPL 117
Db :|||||
Qy 73 RVLRRLPKHKGAVQWRAGSFYFAITVTTTIGYGHAAAPSTDGKVFCMFCFYALLGIPL 132
Db :|||||
Qy 118 TLIMFQSLGERINTFVRYLLHRAKRGGLGMRHAESVMANVVLIGFVSCISTLCIGAAAFSY 177
Db :|||||
Qy 133 TLVMFQSLGERINTSVRYLLHRAKRGGLGMRHAESVMANVVLIGFVSCISTLCIGAAAFSY 192
Db :|||||
Qy 178 YERWTFQAYYYCFITLTTIGFGDYVALQKDQALQTPQVAFSFVYILTGLTVIG--AF 235
Db :|||||
Qy 193 YERWTFQAYYYCFITLTTIGFGDYVALQKDQALQTPQVAFSFVYILTGLTVIG--AF 249
Db :|||||
Qy 236 LNLVLRPMTWNAEDEKRDRAHLLTHNGQAVGLGSLGSLGD-VRPRDPVTCAAA 294
Db :|||||
Qy 295 A 295
Db :|||||
Qy 310 A 310
Db :|||||

RESULT 14
US-09-746-491-61
; Sequence 61, Application US/09746491
; Patent No. US20020137202A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: No. US20020137202A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-621
; CURRENT APPLICATION NUMBER: US/09/746,491
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: USSN 60/171,329
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 61
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-746-491-61

Query Match
Best Local Similarity 99.2%; Score 1306; DB 9; Length 258;
Matches 253; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENVTALIVCTFTYLLVGAAVFDALSEPEMIERQRLRLQLELRARYNLSEGGYEELE 60
Db :|||||
Qy 4 QNVRTALIVCTFTYLLVGAAVFDALSEPEMIERQRLRLQLELRARYNLSEGGYEELE 63
Db :|||||
Qy 61 RVLRRLPKHKGAVQWRAGSFYFAITVTTTIGYGHAAAPSTDGKVFCMFCFYALLGIPLTLI 120
Db :|||||
Qy 64 RVLRRLPKHKGAVQWRAGSFYFAITVTTTIGYGHAAAPSTDGKVFCMFCFYALLGIPLTLV 123
Db :|||||

; PRIOR FILING DATE: 1997-03-11
; PRIOR APPLICATION NUMBER: PCT/US95/14364
; PRIOR FILING DATE: 1995-10-25
; PRIOR APPLICATION NUMBER: 07/332,312
; PRIOR FILING DATE: 1994-10-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 55
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-870-492-55

Query Match
Best Local Similarity 93.0%; Score 1392.5; DB 17; Length 312;
Matches 280; Conservative 2; Mismatches 10; Indels 9; Gaps 4;

Qy 1 ENVTALIVCTFTYLLVGAAVFDALSEPEMIERQRLRLQLELRARYNLSEGGYEELE 60
Db :|||||
Qy 13 ENVTALIVCTFTYLLVGAAVFDALSEPEMIERQRLRLQLELRARYNLSEGGYEELE 72
Db :|||||
Qy 61 RVLRRLPKHKGAVQWRAGSFYFAITVTTTIGYGHAAAPSTDGKV---FCMFYALLGIPL 117
Db :|||||
Qy 73 RVLRRLPKHKGAVQWRAGSFYFAITVTTTIGYGHAAAPSTDGKVFCMFCFYALLGIPL 132
Db :|||||
Qy 118 TLIMFQSLGERINTFVRYLLHRAKRGGLGMRHAESVMANVVLIGFVSCISTLCIGAAAFSY 177
Db :|||||
Qy 133 TLVMFQSLGERINTSVRYLLHRAKRGGLGMRHAESVMANVVLIGFVSCISTLCIGAAAFSY 192
Db :|||||
Qy 178 YERWTFQAYYYCFITLTTIGFGDYVALQKDQALQTPQVAFSFVYILTGLTVIG--AF 235
Db :|||||
Qy 193 YERWTFQAYYYCFITLTTIGFGDYVALQKDQALQTPQVAFSFVYILTGLTVIG--AF 249
Db :|||||
Qy 236 LNLVLRPMTWNAEDEKRDRAHLLTHNGQAVGLGSLGSLGD-VRPRDPVTCAAA 294
Db :|||||
Qy 295 A 295
Db :|||||
Qy 310 A 310
Db :|||||

RESULT 15
US-10-459-190-15
; Sequence 15, Application US/10459190
; Publication No. US20040072216A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Jeffrey D.
; APPLICANT: Palma, John F.
; APPLICANT: Schweitzer, Anthony C.
; APPLICANT: Blume, John E.
; APPLICANT: Metabolex, Inc.
; TITLE OF INVENTION: Methods and Compositions for Treating and Diagnosing
; FILE REFERENCE: 016325-008210US
; CURRENT APPLICATION NUMBER: US/10/459,190
; CURRENT FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: US 60/387,642
; PRIOR FILING DATE: 2002-06-10
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 15
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: transmembrane (TM) and pore domains of mouse
; OTHER INFORMATION: TWIK-related acid-sensitive potassium channel 1
; OTHER INFORMATION: (TASK-1)
US-10-459-190-15

Query Match
Best Local Similarity 99.6%; Score 1200; DB 15; Length 233;
Matches 232; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RTLALIVCTFTYLLVGAAVFDALSEPEMIERQRLRLQLELRARYNLSEGGYEELEERVV 63
Db :|||||
Qy 1 RTLALIVCTFTYLLVGAAVFDALSEPEMIERQRLRLQLELRARYNLSEGGYEELEERVV 60
Db :|||||
Qy 64 LRLPKHKGAVQWRAGSFYFAITVTTTIGYGHAAAPSTDGKVFCMFCFYALLGIPLTIMFQ 123
Db :|||||
Qy 61 LRLPKHKGAVQWRAGSFYFAITVTTTIGYGHAAAPSTDGKVFCMFCFYALLGIPLTIMFQ 120
Db :|||||
Qy 124 SLGERINTFVRYLLHRAKRGGLGMRHAESVMANVVLIGFVSCISTLCIGAAAFSYERWTF 183
Db :|||||
Qy 121 SLGERINTFVRYLLHRAKRGGLGMRHAESVMANVVLIGFVSCISTLCIGAAAFSYERWTF 180
Db :|||||
Qy 184 FQAYYYCFITLTTIGFGDYVALQKDQALQTPQVAFSFVYILTGLTVIGAFGL 236
Db :|||||
Qy 181 FQAYYYCFITLTTIGFGDYVALQKDQALQTPQVAFSFVYILTGLTVIGAFGL 233
Db :|||||

Search completed: September 15, 2005, 22:55:17
Job time : 171 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 16, 2005, 04:35:28 ; Search time 696 Seconds
(without alignments)
3444.677 Million cell updates/sec

Title: US-09-939-483-5
Perfect score: 2105
Sequence: 1 ENVRTALIVCTFYLLVGA.....STGLHSLAFLMKRRSSV 405

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2.1/USPTO_spool/US09939483/runat_15092005_111359_9662/app_query.fasta_1.583
-DB=N_Geneseq_16Dec04 -QFMT=fastap -SUPFIX=ring -MINMATCH=0.1 -LOOPCTL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09939483 @CGN_1.1_644 @runat_15092005_111359_9662 -NCPU=6 -ICPU=3
-NO_MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_16Dec04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1819	86.4	1551	3 AAZ98176	Aaz98176 Human sig
2	1819	86.4	2514	3 AAA27746	Aaa27746 Human pot
3	1819	86.4	2590	12 ADI27914	Adi27914 Human DNA
4	1422	67.6	956	4 AAS12179	Aas12179 Murine 2P
5	1100	52.3	1122	12 ADI27949	Adi27949 Human TWI

6	1100	52.3	1125	3 AAA75886	Aaa75886 cDNA enco
7	1100	52.3	1125	5 AAH74999	Aah74999 Nucleotid
8	1100	52.3	1125	10 ADH34472	Adh34472 Human pot
9	1100	52.3	1248	6 AAD21998	Aad21998 Human tra
10	1100	52.3	1262	6 AAD36247	Aad36247 Human TWI
11	1100	52.3	1262	12 ADI27947	Adi27947 Human TWI
12	1100	52.3	1441	3 AAA75887	Aaa75887 Expressed
13	1100	52.3	2312	5 AAH75002	Aah75002 cDNA sequ
14	1100	52.3	3234	13 ADR65962	Adr65962 Human pro
15	1100	52.3	3234	13 ADR66646	Adr66646 Human pro
16	955.5	45.4	1620	10 ADH34471	Adh34471 Rat potas
17	850.5	40.4	1286	10 ADB80477	Adb80477 Ovarian c
18	850.5	40.4	1528	5 AAD17526	Aad17526 Human TWI
19	850.5	40.4	1528	12 ADI27911	Adi27911 Human TWI
20	843	40.0	1200	12 ADI27913	Adi27913 Human TWI
21	842.5	40.0	1216	4 AAC86163	Aac86163 FCTR11 nu
22	842.5	40.0	1216	10 ADK18421	Adk18421 Human NOV
23	842.5	40.0	1528	5 AAD17525	Aad17525 Human TWI
24	842.5	40.0	1528	12 ADI27908	Adi27908 Human TWI
25	842.5	40.0	2460	6 AAD22005	Aad22005 Human tra
C 26	835	39.7	1113	10 ADK18423	Adk18423 Human NOV
C 27	835	39.7	1113	10 ADK18419	Adk18419 Human NOV
C 28	835	39.7	1113	10 ADK18429	Adk18429 Human NOV
C 29	835	39.7	1200	12 ADI27910	Adi27910 Human TWI
30	779.5	37.0	1434	5 AAS93460	Aas93460 DNA enco
31	773	36.7	1227	4 AAF25380	Aaf25380 Nucleotid
32	753	35.8	1023	4 ABL15117	Ab115117 Drosophil
33	747	35.5	1197	4 ABL29941	Ab129941 Drosophil
C 34	721	34.3	766	4 AAI20418	Aai20418 Probe #10
C 35	721	34.3	766	4 ABA65456	Aba65456 Human foe
C 36	721	34.3	766	4 AAI45622	Aai45622 Probe #14
C 37	721	34.3	766	4 ABA47563	Aba47563 Human bre
C 38	721	34.3	766	4 AAK32553	Aba32553 Probe #11
C 39	721	34.3	766	4 AAK39608	Aak39608 Human bon
C 40	721	34.3	766	4 AAK13864	Aak13864 Human bra
C 41	721	34.3	766	4 ABS39198	Abs39198 Human liv
C 42	721	34.3	766	5 AAI06118	Aai06118 Probe #61
C 43	721	34.3	766	6 ABS13699	Abs13699 Human gen
C 44	713.5	33.9	887	6 ABQ29546	Abq29546 Oligonuc
C 45	713.5	33.9	887	6 ABQ29547	Abq29547 Oligonuc

ALIGNMENTS

RESULT 1
AAZ98176
ID AAZ98176 standard; cDNA; 1551 BP.
AC AAZ98176;
XX
XX
11-MAY-2000 (first entry)
Human signal peptide containing protein HSP-68 cDNA SEQ ID NO:202.
Human; signal peptide-containing protein; HSP; diagnosis; cancer;
inflammation; cardiovascular disease; anticancer; anti-inflammatory;
antimicrobial; neurotropic; neuroprotective; cardiovascular; hepatotropic;
antiasthmatic; gene therapy; cell proliferation; neurological disorder;
reproductive disorder; developmental disorder; arteriosclerosis;
cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
Parkinson's disease; Huntington's diseases; ovulatory defect;
muscular dystrophy; ss.
Homo sapiens.
OS
XX
XX
FN WO200000610-A2.
XX
XX
06-JAN-2000.
PD
XX
XX
25-JUN-1999; 99WO-US014484.
PF
XX
XX
26-JUN-1998; 98US-0090762P.
PR

Db 1233 GCCATCAGTCGGTGTCCACGGGTCTGCACAGCCTGTCCACCTTCGCGGCTCATGAAG 1292
Qy 401 ArgArgSerSerVal 405
Db 1293 CGCAGGAGCTCCGGT 1307
RESULT 3
ID ADI27914
ID ADI27914 standard; DNA; 2590 BP.
XX AC ADI27914;
XX DT 06-MAY-2004 (first entry)
XX DE Human DNA #1.
XX KW Human; gene; ds; ion channel family; ICF; cancer; leukaemia;
KW Alzheimer's disease; Parkinson's disease; multiple sclerosis; epilepsy;
KW hepatic disorder; cardiovascular disorder; cytostatic; neuroprotective;
KW neurotic; antiparkinsonian; hepatotropic; cardiovascular.
XX OS Homo sapiens.
XX PN US2003165891-A1.
XX PD 04-SEP-2003.
XX PF 15-MAY-2002; 2002US-00146733.
XX PR 29-FEB-2000; 2000US-00515520.
PR 29-FEB-2000; 2000US-0185938P.
PR 03-MAR-2000; 2000US-00518966.
PR 07-APR-2000; 2000US-0195734P.
PR 11-APR-2000; 2000US-0195993P.
PR 26-APR-2000; 2000US-0199799P.
PR 19-SEP-2000; 2000US-0233537P.
PR 25-SEP-2000; 2000US-0235018P.
PR 25-SEP-2000; 2000US-0235059P.
PR 15-DEC-2000; 2000US-0256240P.
PR 18-DEC-2000; 2000US-0256588P.
PR 21-DEC-2000; 2000US-0258028P.
PR 06-APR-2001; 2001US-00796720.
PR 11-APR-2001; 2001US-00833081.
PR 25-APR-2001; 2001US-00843328.
PR 19-SEP-2001; 2001US-00957683.
PR 25-SEP-2001; 2001US-00964252.
PR 17-DEC-2001; 2001US-00024623.
XX (MILL-) MILLENNIUM PHARM INC.
XX PA Curtis RAJ, Glucksmann MA, Silos-Santiago I;
XX FI WPI; 2004-069000/07.
XX DR TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9,
XX PT alphasdelta-4, 54414, or 53763 nucleic acids and proteins, useful for
XX FT preventing, diagnosing and treating e.g. cancers, Alzheimer's disease and
XX PT cardiovascular disorders.
XX PS Disclosure; SEQ ID NO 7; 638pp; English.
XX CC The invention relates to TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611,
CC IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and 53763 ion channel
CC family (ICF) nucleic acids and proteins. The TWIK-6, TWIK-7, IC23927,
CC TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and
CC 53763 ICF nucleic acids and proteins may be used for preventing,
CC diagnosing and treating ICF-related diseases. The sequences may be used
CC to treat disorders associated with decreased expression by rectifying
CC mutations or deletions in a patient's genome that affect the activity of
CC ICF proteins by expressing inactive proteins or to supplement the

CC patients own production of ICF proteins. The proteins may also be used as
CC antigens in the production of antibodies against ICF proteins and in
CC assays to identify modulators of ICF protein expression and activity. The
CC anti-ICF protein antibodies, agonists and antagonists may be used to
CC regulate ICF protein expression and activity. The antibodies may also be
CC used as diagnostic agents for detecting the presence of ICF proteins in
CC samples (e.g. by immunoassay). The nucleic acids and proteins may be used
CC to prevent, diagnose and treat a wide variety of disorders, e.g. cancers
CC and leukaemia. Alzheimer's disease, Parkinson's disease, multiple
CC sclerosis, epilepsy, hepatic disorders and cardiovascular disorders. This
CC sequence represents human DNA used in the scope of the invention. Note:
CC The sequence data for this patent is also available in electronic format
CC from USPTO at segdata.uspto.gov/sequence.html.
XX SQ Sequence 2590 BP; 502 A; 829 C; 789 G; 470 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 6,78e-184 Length: 2590
Score: 1819.00 Matches: 357
Percent Similarity: 90.37% Conservative: 9
Best Local Similarity: 88.15% Mismatches: 25
Query Match: 86.41% Indels: 14
DB: 12 Gaps: 2
US-09-939-483-5 (1-405) x ADI27914 (1-2590)
Qy 1 GluAenValArgThrLeuAlaLeuIleValCyeThrPheThrTyrLeuLeuValGlyAla 20
Db 135 CAGAACGTGCGCACGCTGGCGCTCATCGTGTGCACCTTACCTTACCTGTGGTGGCGCC 194
Qy 21 AlaValPheAspAlaLeuGluSerGluProGluMetIleGluArgGlnArgLeuLeu 40
Db 195 GCGGTCTTCGACGCGCTGGAGTCGGAGCCGAGCTGATCAGCGCGCAGCGCTGGAGTG 254
Qy 41 ArgGlnLeuGluLeuArgAlaArgTyrAsnLeuSerGluGlyGlyTyrGluLeuLeuGlu 60
Db 255 CGGCAGCAGGAGCTGCGCGCGCTACAACCTCAGCCAGCGCGCTACGAGGAGCTGGAG 314
Qy 61 ArgValValLeuArgLeuLysProHisLysAlaGlyValGlnTrpArgPheAlaGlySer 80
Db 315 CGCGTGTGCTGGCGCTCAAGCCGCAAGCGCGGTGCAGTGGCGCTTCGCGCGCTCC 374
Qy 81 PheTyrPheAlaIleThrValIleThrIleGlyTyrGlyHisAlaAlaProSerThr 100
Db 375 TTCTACTTGGCCATCACCCTGTCATCACCCTGCTAGCGGCACGCGGCAGCCAGCAGC 434
Qy 101 AspGlyGlyLysValPheCysMetPheTyrAlaLeuLeuGlyIleProLeuThrLeuIle 120
Db 435 GATGGCGCAAGGTGTCTGCATGTTCTAGCGCTCTGCGGCATCCGCTCAGCGCTCGTC 494
Qy 121 MetPheGlnSerLeuGlyGluArgIleAsnThrPheValArgTyrLeuLeuHisArgAla 140
Db 495 ATGTTCCAGAGCCTGGCGGAGCGCATCAACCTTGTGTAGGTACTCTGTGCACCGCGCC 554
Qy 141 LysArgGlyLeuGlyMetArgHisAlaGluValSerMetAlaAsnMetValLeuIleGly 160
Db 555 AAGAAGGGCTGGGCATGGCGCGCGCGCTGCTCCATGGCCAAATGTTGTCTCATCGGC 614
Qy 161 PheValSerCysIleSerThrLeuCysIleGlyAlaAlaPheSerTyrTyrGluArg 180
Db 615 TTCTTCTGTGTCATCAGCAGCTGTGCATCGCGCGCGCTCTCCCACTACGTAGTTC 674
Qy 181 TrpThrPhePheGlnAlaTyrTyrCysPheIleThrLeuThrThrIleGlyPheGly 200
Db 675 TGGACCTTCTTCAGGCGCTACTACTGTTTATCCTCACCCTCACCACCTCGGCTTCGGC 734
Qy 201 AspTyrValAlaLeuGlnLysAspGlnAlaLeuGlnThrGlnProGlnTyrValAlaPhe 220
Db 735 GACTACGTGGCGCTGCAGAGGACAGCGCTCAGACGCGCGCGCTACGTAGTTCGCTTC 794
Qy 221 SerPheValTyrIleLeuThrGlyLeuThrValIleGlyAlaPheLeuAenLeuValVal 240
Db 795 AGCTTCGTCTACATCTTACGGGCGCTCAGCGTTCATCGGCGCTTCCTCAACCTCGTGGT 854

QY 241 LeuArgPheMetThrMetAsnAlaGluAspGluIysArgAspAlaGluHisArgAlaLeu 260
 Db 855 CTGGCGCTTCATGACCATGACCGGAGGACGAGAGCGCGCGAGCACCGCGCGCTG 914
 QY 261 LeuThrHisAsnGlyGlnAlaValGlyLeuGlyGlyLeuSerCysLeuSerGlySerLeu 280
 Db 915 CTCAGCGCAACGGGACGGCGGGCGCGCGGAGG-----GGT 953
 QY 281 GlyAspValArgProArgAspProValThrCysAlaAlaAlaGlyGlyValGlyVal 300
 Db 954 GGCAGCGGCACACTACGACACCGCCTCATCCAGCGCGGAGG----- 998
 QY 301 GlyValGlyGlySerGlyPheArgAsnValTyrAlaGluValLeuHisPheGlnSerMet 320
 Db 999 -----GGCGGGCGGGCTTCGCAACGCTACGCGGAGGTGCTGCACCTCCAGTCCATG 1052
 QY 321 CysSerCysLeuTyrTyrLysSerArgGluIysLeuGlnTyrSerIleProMetIleIle 340
 Db 1053 TGCTCGTGCCTGTGTATACAGAGCGCGGAGAGCTGCAGTACTCATCCCCATGATCATC 1112
 QY 341 ProArgAspLeuSerThrSerAspThrCysValGluHisSerHisSerSerProGlyGly 360
 Db 1113 CGCGGGACCTCTCCACGTCCGACACGTCGTCGTGGAGCAGAGCCACTCGTCGCGGGAGG 1172
 QY 361 GlyGlyArgTyrSerAspThrProSerHisProCysLeuCysSerGlyThrGlnArgSer 380
 Db 1173 GCGCGCCGCTACAGCAGACACGCCCTCGCGAGCGCTGCTGTGCGCGGGCGCCACGCTCC 1232
 QY 381 AlalSerSerValSerThrGlyLeuHisSerLeuAlaAlaPheArgGlyLeuMetIys 400
 Db 1233 GCCATCAGCTCGGTGTCCAGGGGTGTCACAGCCTGTCCACCTTCCTCGCGGGCTCATGAAG 1292
 QY 401 ArgArgSerSerVal 405
 Db 1293 CGCAGGAGCTCGGTG 1307

RESULT 4
 AAS12179
 ID AAS12179 standard; cDNA; 956 BP.
 XX
 AC AAS12179;
 XX
 DT 21-NOV-2001 (first entry)
 XX
 DE Murine 2P channel cDNA clone #1.
 XX
 KW Transmembrane potassium ion channel protein; inward potassium flux; ss;
 KW pest control; membrane potential; pesticide; antihelminthic; nematode;
 KW insect; 2P channel; mouse.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT CDS 30..956
 FT /*tag= a
 FT /product= "Mouse 2P channel protein #1"
 XX
 PN WO200161006-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 14-FEB-2001; 2001WO-US004680.
 XX
 PR 15-FEB-2000; 2000US-00503849.
 XX
 PA (BADI) BASF CORP.
 XX
 PI Pausch MH;
 XX
 DR WPI; 2001-536570/59.
 DR P-PSDB; AAU07620.
 XX

PT New polypeptide, a mutant potassium ion channel protein for improving
 XX inward potassium flux under acidic conditions.

PS Example 18; Page 52-53; 131pp; English.

XX The invention relates to a mutant potassium ion channel protein, having
 CC four membrane spanning domains and two pore forming domains, comprising a
 CC mutation at the second pore forming domain. The expression of the mutant
 CC protein in a cell confers improved inward potassium flux and the ability
 CC to grow in the presence of potassium. Mutant proteins and their
 CC corresponding polynucleotide sequences can therefore be used to improve
 CC inward potassium flux into cells under acidic conditions by modulating
 CC the membrane potential using therapeutic agents. The sequences may be
 CC used to develop agonists and antagonists of potassium channel proteins in
 CC order to control pests such as nematodes and insects. This sequence
 CC represents a mouse cDNA encoding a 2P channel protein

SQ Sequence 956 BP; 168 A; 304 C; 298 G; 186 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4,85e-142 Length: 956
 Score: 1422.00 Matches: 290
 Percent Similarity: 98.31% Conservative: 1
 Best Local Similarity: 97.97% Mismatches: 4
 Query Match: 67.55% Indels: 4
 DB: 4 Gaps: 1

US-09-939-483-5 (1-405) x AAS12179 (1-956)

QY 1 GluAsnValArgThrLeuAlaLeuIleValCysThrPheThrTyrLeuLeuValGlyAla 20

Db 66 GAGAAATGTGGCGAGTGTGGCTCTCATGTGTGACCTTCACCTACCTGTGTGGGGCGCC 125

QY 21 AlaValPheAspAlaLeuGluSerGluProGluMetIleGluArgGlnArgLeuLeu 40

Db 126 GCGGTGTTTCAGCACCTGGAGTCGGAGCGGAGATGATCAGCGGCGGCTGGAGCTG 185

QY 41 ArgGlnLeuGluLeuArgAlaArgTyrAsnLeuSerGluGlyTyrGluGluLeuGlu 60

Db 186 CGGCAGCTGGAGCTGGCGGGCGCTACAACCTCAGCGAGGGCGGCTACGAGGAGCTGGAG 245

QY 61 ArgValValLeuLeuArgLeuLysProHisLysAlaGlyValGlnTyrArgPheAlaGlySer 80

Db 246 CGGTGCTGTGCGCTCAAGCCGACACAGCGCGGTGCGAGTGGCGCTTCGCGGGCTCC 305

QY 81 PheTyrPheAlaIleThrValIleThrThrIleGlyTyrGlyHisAlaAlaProSerThr 100

Db 306 TTCTACTTCGCCATCACCCTCATCCACCATCGGCTATGTCATGCGGCGCCGAGCAGC 365

QY 101 AspGlyGlyLysValPheCysMetPheTyrAlaLeuLeuGlyIleProLeuThrLeuIle 120

Db 366 GACGGAGGCAAGGTGTTCTCATGCGCTGTGGGCGATCCCGCTCACACTAGTC 425

QY 121 MetPheGlnSerLeuGlyGluArgIleAsnThrPheValArgTyrLeuLeuHisArgAla 140

Db 426 ATGTTCCAGAGCTGGGTGAACGATCAACCTCCGTGAGGTACCTGTGCACCGCTGCC 485

QY 141 LysArgGlyLeuGlyMetArgHisAlaGluValSerMetAlaAsnMetValLeuIleGly 160

Db 486 AAGAGGGGGCTGGGCATGGCGCAGCGGAGTGTCCATGCCAACATGGTGCTCATCGGT 545

QY 161 PheValSerCysIleSerThrLeuCysIleGlyAlaAlaAlaPheSerTyrTyrGluArg 180

Db 546 TTCGTGTGTGCATCAGCAGCTGTGCATGCGGCGAGCTGCCTTCTCTACTACGAGCGC 605

QY 181 TrpThrPhePheGlnAlaTyrTyrCysPheIleThrLeuThrThrIleGlyPheGly 200

Db 606 TGGACTTTCTTCCAGGCTATTACTGCTTATCACCTCCACCATCGGCTTCGGCTTCGGC 665

QY 201 AspTyrValAlaLeuGlnLysAspGlnAlaLeuGlnThrGlnProGlnTyrValAlaPhe 220

Db 666 GACTATGTGGCGCTGCAGAGGACCGAGCGCTGCAGACGCGCGGCGCATGTGTGGC-TTC 724


```
QY 161 PheValSerCysIleSerThrLeuCysIleGlyAlaAlaAlaPheSerTyrTyrGluArg 180
Db 490 TTCTTCTCTGCAATGGGAGCGTGTGATCGGGCGGCCCTCTCCAGTGTGAGAG 549
QY 181 TrpThrPhePheGlnAlaTyrTyrCysPheIleThrLeuThrThrIleGlyPheGly 200
Db 550 TGGAGCTTCTCCACGCGCTACTACTACTGCTTATCAGTTGACTACCATTTGGTTGGG 609
QY 201 AspTyrValAlaLeuGlnLysAspGlnAlaLeuGlnThrGlnProGlnTyrValAlaPhe 220
Db 610 GACTACGTGGCCCTGACAGCAAGGCGGCCCTGACAGAAAGCGCTCTACTGTCGCTTT 669
QY 221 SerPheValTyrIleLeuThrGlyLeuThrValIleGlyAlaPheLeuLeuValVal 240
Db 670 AGCTTATGATATCTCTGTTGGGCTGACGCTATCGGGGCTTCTCAACCTGGTCGTC 729
QY 241 LeuArgPheMetThrMetAsnAlaGluAspGluLysArgAspAlaGluHisArgAlaLeu 260
Db 730 CTCAGGTTCTTGACCATGAACATGAGATGAGCGGGGATGCTGAAGAGAGGCGATCC 789
QY 261 LeuThrHisGlnGlnAlaValGlyLeuGlyCysLeuSerCysLeuSerGlySerLeu 280
Db 790 CTGCGCGGAACCGCAAC-----AGCATGGTCAATTCACATCCCT 828
QY 281 GlyAspValArgProArgAspProValThrCysAlaAlaAlaGlyGlyValGlyVal 300
Db 829 GAGAGCGCGCGCCAGCCGCGCC-----852
QY 301 GlyValGlySerGlyPheArgAsnValTyrAlaGluValLeuHisPheGlnSerMet 320
Db 853 -----AGGTACAAGCGGACGCTCCGGACCTGCGAGTCTGTG 888
QY 321 CysSerCysLeuTrpTyrLysSerArgGluLysLeuGlnTyrSerIleProMetIleIle 340
Db 889 TGTCTCTGCACTGCTACCGCTCGCAGAC-----TATGGCGCGCGCTCGTGCA 939
QY 341 ProArgAspLeuSerThrSerAspThrCysValGluHisSerHisSer-----356
Db 940 CCGCAGACTCTCTCAGCGCAAGCTGGCCCCCCTATTCACATCCATCTCTTACAAG 999
QY 357 -----SerProGlyGlyGlyArgTyrSerAspThrProSerHisProCys 372
Db 1000 ATCGAGGAGATCTCACCAAGC-----ACA 1023
QY 373 LeuCysSerGlyThrGlnArgSerAlaIleSerSerValSerThrGlyLeuHisSerLeu 392
Db 1024 TTAATAAACAGCCTCTTCCCATCGCTATTAGTCCATCTCTCTGGTTTACAGCTTT 1083
QY 393 AlaAlaPheArgGlyLeuMetLysArgArgSerSerVal 405
Db 1084 ACCGACCACCAGAGGCTGATGAACCGCGGAAGTCTCGTT 1122
```

```
RESULT 7
AAH74999
ID AAH74999 standard; DNA; 1125 BP.
XX
AC AAH74999;
XX
XX 29-OCT-2001 (first entry)
DT
XX Nucleotide sequence of human potassium channel protein KCNB.
DE
XX Human; potassium channel protein; KCNB; breast tissue; cancer; stroke;
KW potassium channel-associated disorder; brain associated disorder;
KW epilepsy; Alzheimer's disease; Parkinson's disease; multiple sclerosis;
KW migraine; psychiatric disorder; depression; schizophrenia; diabetes;
KW bipolar disease; heart disease; arrhythmia; pancreas disease;
KW pancreatitis; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
, FH
```

```
FT CDS 1. .1125
FT /tag= a
FT /product= "potassium channel protein KCNB"
XX
PN WO200166741-A2.
PD 13-SEP-2001.
XX
PF 02-MAR-2001; 2001WO-US006801.
XX
PR 03-MAR-2000; 2000US-0186915P.
XX
PA (TULA-) TULARIK INC.
XX
PI Mu D, Powers S;
XX
DR WPI; 2001-522949/57.
DR P-PSDB; AAG63938.
XX
PT A nucleic acid encoding a potassium channel, termed KCNB (potassium channel expressed in breast), useful in the diagnosis, prognosis or treatment of diseases associated with altered KCNB activity or expression, e.g. cancer and diabetes.
XX
PS Claim 6; Page 79-80; 82pp; English.
XX
XX The present sequence encodes a human potassium channel protein, termed KCNB. KCNB is expressed in breast tissue. The KCNB polypeptides are useful for identifying a compound that modulates its activity. The KCNB polypeptide and nucleic acid are useful for detecting cancer cells in biological samples. The inhibitor of the potassium channel polypeptide is useful for inhibiting proliferation of a cancer cell and for treating a potassium channel-associated disorder. The KCNB nucleic acids, proteins, and/or antibodies are useful in the diagnosis or prognosis, or treatment of diseases associated with altered KCNB activity or expression. Such diseases are cancer, brain associated disorders (such as epilepsy, Alzheimer's disease, Parkinson's disease, stroke, multiple sclerosis, migraine), psychiatric disorders (such as depression, schizophrenia, bipolar diseases) and diseases related to the heart (such as arrhythmias), diseases related to pancreas (such as pancreatitis and diabetes)
XX
SQ Sequence 1125 BP; 227 A; 348 C; 319 G; 231 T; 0 U; 0 Other;
```

```
Alignment Scores:
Pred. No.: 1.89e-107 Length: 1125
Score: 1100.00 Matches: 229
Percent Similarity: 67.07% Conservative: 48
Best Local Similarity: 55.45% Mismatches: 86
Query Match: 52.26% Indels: 50
DB: Gaps: 5
```

```
US-09-939-483-5 (1-405) x AAH74999 (1-1125)
QY 1 GluAsnValArgThrLeuAlaLeuValCysThrPheThrTyrLeuValGlyAla 20
Db 10 CAGAGCTGGGAGCTCTGCTCCCTCATCTCTGACCTTACCTACCTGTTGGGGGCC 69
QY 21 AlaValPheAspAlaLeuGluSerGluProGluMetIleGluArgGlnArgLeuGluLeu 40
Db 70 GCGGTGTTCCAGCGCCCTCGAGTCGGACACGAGATCGCGGAGGAGAACTCAAAGCC 129
QY 41 ArgGlnLeuGluLeuArgAlaArgTyrAsnLeuSerGluGlyClyTyrGluGluLeuGlu 60
Db 130 GAGGAGATCCGATCAAGGGGAAGTACAACATCAGCAGCGAGGACTACCGGAGCTGGAG 189
QY 61 ArgValValLeuArgLeuLysProHisLysAlaGlyValGlnTrpArgPheAlaGlySer 80
Db 190 CTGCTGATCTGCTGAGTCGGAACCGCACCGCGCGGCTCCAGTGGAAATTCGCGGCTCC 249
QY 81 PheTyrPheAlaIleThrValIleThrIleGlyTyrGlyHisAlaAlaProSerThr 100
Db 250 TTCTACTTTCGATCAGCGTTCATCACCACATAGGTATATGGGCACGCTGCACCTGGCACC 309
```

```
Qy 101 AspGlyGlyLysValPheCysMetPheTyrAlaLeuLeuGlyIleProLeuThrLeuIle 120
Db 310 GATGGGCAAGGCTTCTGATGTTACGCGGTGCTGGCATCCCGCTGACACTGGTC 369
Qy 121 MetPheGlnSerLeuGlyGluArgIleAsnThrPheValArgTyrLeuLeuHisArgAla 140
Db 370 ATGTTCCAGACCTGGGGAGCGCATGAACACCTTCGTGGCGCTACCTGCTGAAGCGATT 429
Qy 141 LysArgGlyLeuGlyMetArgHisAlaGluValSerMetAlaAsnMetValLeuIleGly 160
Db 430 AAGAAGTCTGTGGCATCGCAACACTGACGTGTATGAGAGACATGGTCACTGGGC 489
Qy 161 PheValSerCysIleSerThrLeuCysIleGlyAlaAlaAlaPheSerTyrTyrGluArg 180
Db 490 TTCTTCTCTCATGGGACGCTGTGCATCGGGCGCGCGCTTCCTCCAGTGTGAGAG 549
Qy 181 TrpThrPhePheGlnAlaTyrTyrTyrCysPheIleThrLeuThrThrIleGlyPheGly 200
Db 550 TGGAGCTTCTTCCAGCGCTACTACTACTGCTTCATCAGTTGACTTACCATTTGGGTTCGG 609
Qy 201 AspTyrValAlaLeuGlnLysAspGlnAlaLeuGlnThrGlnProGlnTyrValAlaPhe 220
Db 610 GACTACGTGGCCCTGCAGACCAAGGTCCTCTGCAGAAAGACGCTCTACGTGGCCTTT 669
Qy 221 SerPheValTyrIleLeuThrGlyLeuThrValIleGlyAlaPheLeuAsnLeuValVal 240
Db 670 AGCTTTATGTATATCTGTGGGCTGACGCTCATCGGGGCTTCCTCAACCTGTCGTC 729
Qy 241 LeuArgPheMetThrMetAsnAlaGluAspGluLysArgAspAlaGluHisArgAlaLeu 260
Db 730 CTCAGGTTCTTGACCATCAAGCAGGAGTGGGGGATGCTGAAGAGAGGAGGCAATCC 789
Qy 261 LeuThrHisAsnGlyGlnAlaValGlyLeuGlyLeuSerCysLeuSerGlySerLeu 280
Db 790 CTCGCGGAACCGCAAC-----ACATGGTCATTTCACATCCCT 828
Qy 281 GlyAspValArgProArgAspProValThrCysAlaAlaAlaGlyValGlyVal 300
Db 829 GAGGAGCGCGCGCGCGCGCC-----852
Qy 301 GlyValGlyGlySerGlyPheArgAsnValTyrAlaGluValLeuHisPheGlnSerMet 320
Db 853 -----AGTTACAAGCGCGACGTCCTCGGACCTGCACTCTGTG 888
Qy 321 CysSerCysLeuTyrTyrLysSerArgGluLysLeuGlnTyrSerIleProMetIleIle 340
Db 889 TGCTCTGCACTGCTACCGCTCGCAGAC-----TATGGCGCGCTCGGTGGCA 939
Qy 341 ProArgAspLeuSerThrSerAspThrCysValGluHisSerHisSer-----356
Db 940 CCGCAGAACCTCTTCAGCGCAAGCTTGCCCCCACTACTTCCACTCCATCTCTTACAAG 999
Qy 357 -----SerProGlyGlyGlyGlyArgTyrSerAspThrProSerHisProCys 372
Db 1000 ATCAGAGAGATCTCACCAAGC-----ACA 1023
Qy 373 LeuCysSerGlyThrGlnArgSerAlaIleSerSerValSerThrGlyLeuHisSerLeu 392
Db 1024 TTAACAAACAGCTCTTCCCATCGCTTATAGCTCCATCTCTCTGGGTTACAGCTTT 1083
Qy 393 AlaAlaPheArgGlyLeuMetLysArgSerSerVal 405
Db 1084 ACCGACCAACAGAGGCTGATGAACCGCGGAATCCGTT 1122
RESULT 8
ID ADH34472 standard; cDNA; 1125 BP.
XX AC ADH34472;
XX XT 11-MAR-2004 (first entry)
XX
```

Human potassium channel TASK-3-encoding cDNA.

Human; TASK-3; potassium channel; K⁺ channel; outwardly rectifying; acid-sensitve; central nervous system; nociception; chronic pain; diabetic neuropathy; postherpetic neuralgia; fibromyalgia; surgery; chronic back pain; analgesic; gene therapy; antisense therapy; gene; ss.

Homo sapiens.

DE	Key	Location/Qualifiers
XX	misc_binding	55..70
FT		/*tag= a
FT		/bound_moiety= "Human TASK-3 antisense oligonucleotide"
FT	misc_binding	101..156
FT		/*tag= b
FT		/bound_moiety= "Human TASK-3 antisense oligonucleotide"
FT	misc_binding	163..194
FT		/*tag= c
FT		/bound_moiety= "Human TASK-3 antisense oligonucleotide"
FT	misc_binding	226..240
FT		/*tag= d
FT		/bound_moiety= "Human TASK-3 antisense oligonucleotide"
FT	misc_binding	305..322
FT		/*tag= e
FT		/bound_moiety= "Human TASK-3 antisense oligonucleotide"
FT	misc_binding	434..443
FT		/*tag= f
FT		/bound_moiety= "Human TASK-3 antisense oligonucleotide"
FT	misc_binding	481..489
FT		/*tag= g
FT		/bound_moiety= "Human TASK-3 antisense oligonucleotide"
FT	misc_binding	500..512
FT		/*tag= h
FT		/bound_moiety= "Human TASK-3 antisense oligonucleotide"
FT	misc_binding	515..524
FT		/*tag= i
FT		/bound_moiety= "Human TASK-3 antisense oligonucleotide"
FT	misc_binding	540..557
FT		/*tag= j
FT		/bound_moiety= "Human TASK-3 antisense oligonucleotide"
FT	misc_binding	595..615
FT		/*tag= k
FT		/bound_moiety= "Human TASK-3 antisense oligonucleotide"
FT	misc_binding	641..658
FT		/*tag= l
FT		/bound_moiety= "Human TASK-3 antisense oligonucleotide"
FT	misc_binding	685..696
FT		/*tag= m
FT		/bound_moiety= "Human TASK-3 antisense oligonucleotide"
FT	misc_binding	700..711
FT		/*tag= n
FT		/bound_moiety= "Human TASK-3 antisense oligonucleotide"
FT	misc_binding	775..786
FT		/*tag= o
FT		/bound_moiety= "Human TASK-3 antisense oligonucleotide"
FT	misc_binding	791..806
FT		/*tag= p
FT		/bound_moiety= "Human TASK-3 antisense oligonucleotide"
FT	misc_binding	829..837
FT		/*tag= q
FT		/bound_moiety= "Human TASK-3 antisense oligonucleotide"
FT	misc_binding	929..947
FT		/*tag= r
FT		/bound_moiety= "Human TASK-3 antisense oligonucleotide"
FT	misc_binding	998..1013
FT		/*tag= s
FT		/bound_moiety= "Human TASK-3 antisense oligonucleotide"
FT	misc_binding	1088..1102
FT		/*tag= t
FT		/bound_moiety= "Human TASK-3 antisense oligonucleotide"
FT	misc_binding	1108..1116
FT		/*tag= u
FT		/bound_moiety= "Human TASK-3 antisense oligonucleotide"

XX WO2003057846-A2.
 XX 17-JUL-2003.
 XX 31-DEC-2002; 2002WO-US041834.
 XX 31-DEC-2001; 2001US-0346070P.
 XX (ALGO-) ALGOS THERAPEUTICS INC.
 XX Shuster SJ, Arvidsson UNG, Stone LS, Zhang H, Hart LV;
 XX WPI; 2003-587116/55.
 XX New isolated antisense oligonucleotides specifically hybridizing with an
 PT accessible region of TASK-3 mRNA, useful for modulating pain from
 PT diabetic neuropathy, postherpetic neuralgia, fibromyalgia, surgery or
 PT chronic back pain.
 XX Claim 4; SEQ ID NO 2; 37pp; English.
 XX The invention relates to antisense oligonucleotides 10-50 bases in length
 CC targeted to rat or human TASK-3 mRNA (corresponding cDNAs shown in
 CC ADH34471-ADH34472). TASK-3 is an outwardly rectifying acid-sensitive
 CC potassium channel which is regulated by extracellular pH. It is mainly
 CC expressed in central nervous system tissue in regions implicated in
 CC nociception and chronic pain, indicating that it may have a role in pain
 CC sensation. The invention also relates to compositions comprising the
 CC antisense oligonucleotides; a nucleic acid construct and host cell
 CC comprising a regulatory element operably linked to a nucleic acid
 CC molecule that can be transcribed to form an antisense RNA; use of the
 CC antisense oligonucleotides in decreasing TASK-3 production; and a method
 CC of screening for compounds that modulate TASK-3 expression. The antisense
 CC oligonucleotides and compounds are useful for modulating pain, preferably
 CC from diabetic neuropathy, postherpetic neuralgia, fibromyalgia, surgery,
 CC or chronic back pain. The present sequence represents human TASK-3 cDNA.
 XX
 XX Sequence 1125 BP; 227 A; 348 C; 319 G; 231 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.89e-107 Length: 1125
 Score: 1100.00 Matches: 229
 Percent Similarity: 67.07% Conservative: 48
 Best Local Similarity: 55.45% Mismatches: 86
 Query Match: 52.26% Indels: 50
 DB: 10 Gaps: 5
 US-09-939-483-5 (1-405) x ADH34472 (1-1125)
 QY 1 GluAsnValArgThrLeuAlaLeuValCysThrPheThrTyrLeuLeuValGlyAla 20
 Db 10 CAGAACGTGGCGACTGTCTCCCTCATCGTTCACCTTACCTACCTGTGGTGGCGCC 69
 QY 21 AlaValPheAspAlaLeuGluSerGluProGluMetIleGluArgGlnArgLeuGluLeu 40
 Db 70 GCCGTGTTCCAGCCCTCGAGTCGACACGATGCGCGAGGAGAACTCAAGCC 129
 QY 41 ArgGlnLeuGluLeuArgAlaArgTyrAsnLeuSerGluGlyTyrGluGluLeuGlu 60
 Db 130 GAGGAGATCGCGATCAAGGGGAGATCAACATCAGCAGCGAGGACTACCGCGAGTGGAG 189
 QY 61 ArgValValLeuArgLeuLeuProHisLeuAlaGlyValGlnTrpArgPheAlaGlySer 80
 Db 190 CTGGTGAATCTGCAAGTCGGAACCGCACCGCGCGCTCAGTGGAAATTCGCGCGCTCC 249
 QY 81 PheTyrPheAlaIleThrValIleThrThrIleGlyTyrGlyHisAlaAlaProSerThr 100
 Db 250 TTCTACTTTGGATCAGCGTCATCACCACCATAGTTATGGCACGCTGCACCTGGGCACC 309
 QY 101 AspGlyGlyValPheCysMetPheTyrAlaLeuLeuGlyIleProLeuThrLeuLeu 120
 Db 310 GATCGCGGCAAGGCTTCTGTCATGTTCTACGCGGTGCTGGGCATCCCGCTGACACTGGTC 369

QY 121 MetPheGlnSerLeuGluArgIleAsnThrPheValArgTyrLeuLeuHisArgAla 140
 Db 370 ATGTTCCAGAGCCTGGCGAGCGCATGACACCTTCGTGGCTTACTGCTGAAGCGCAT 429
 QY 141 LysArgGlyLeuGlyMetArgHisAlaGluValSerMetAlaAsnMetValLeuIleGly 160
 Db 430 AAGAAGTGTGTGGCATGCGCAACTGACGTGCTATGAGAAACATGGTGAAGTGGGC 489
 QY 161 PheValSerCysIleSerThrLeuCysIleGlyAlaAlaPheSerTyrTyrGluArg 180
 Db 490 TTCTTCTCTGATGGGAGCGCTGTCATCGGGCGCGCTTCTCCAGTAGTGGAG 549
 QY 181 TrpThrPheGlnAlaTyrTyrCysPheIleThrLeuThrThrIleGlyPheGly 200
 Db 550 TGGAGCTTCTTCACCGCTTACTACTGCTTCTCATCAGTTGACTACCATTTGGGTTCGGG 609
 QY 201 AspTyrValAlaLeuGlnLysAspGlnAlaLeuGlnThrGlnProGlnTyrValAlaPhe 220
 Db 610 GACTACGTGGCCCTGCAGACCAAGGCTGCCCTGCAGAAAGCCGCTTACGTGGCCTTT 669
 QY 221 SerPheValTyrIleLeuThrGlyLeuThrValIleGlyAlaPheLeuLeuValVal 240
 Db 670 AGCTTTATGTATATCTGCTGGGCTGCAGGCTCATCGGGCCCTTCTCAACCTGGTCGTC 729
 QY 241 LeuArgPheMetThrMetAsnAlaGluAspGluLysArgAspAlaGluHisArgAlaLeu 260
 Db 730 CTCAGTTCTTGACCATGAACAGTGAGGATGACGGCGGATGCTGAAGAGGGGATCC 789
 QY 261 LeuThrHisAsnGlyGlnAlaValGlyLeuGlyLeuSerCysLeuSerGlySerLeu 280
 Db 790 CTCGCCGAAACCGCAAC-----AGCATGGTTCATTTCATCATCCCT 828
 QY 281 GlyAspValArgProArgAspProValThrCysAlaAlaAlaGlyGlyValGlyVal 300
 Db 829 GAGGAGCCCGCGCCAGCCGCGCC-----852
 QY 301 GlyValGlyGlySerGlyPheArgAsnValTyrAlaGluValLeuHisPheGlnSerMet 320
 Db 853 -----AGGTACAGCGGAGCGTCCCGGACCTGCAGTCTGTG 888
 QY 321 CysSerCysLeuTrpTyrLysSerArgGluLysLeuGlnTyrSerIleProMetIleIle 340
 Db 889 TGCTCTCTGCACCTGTCTACCGCTCGCAGGAC-----TATGGCGCGCGCTCGGTGGCA 939
 QY 341 ProArgAspLeuSerThrSerAspThrCysValGluHisSerHisSer-----356
 Db 940 CCGCAGAACTCTTCAGCGCCAAAGCTTGCCCCCCTACTTCCACTTCCATCTCTTACAAG 999
 QY 357 -----SerProGlyGlyGlyArgTyrSerAspThrProSerHisProCys 372
 Db 1000 ATCGAGGAGATCTCACAACG-----ACA 1023
 QY 373 LeuCysSerGlyThrGlnArgSerAlaIleSerSerValSerThrGlyLeuHisSerLeu 392
 Db 1024 TTAATAAACAGCGCTCTCCCATCGCTATTAGTCCATCTCTCTGGGTTACACAGCTTT 1083
 QY 393 AlaAlaPheArgGlyLeuMetLysArgArgSerSerVal 405
 Db 1084 ACCGACCAACGAGGCTGATGAACCCGGAAGTCCGTT 1122
 RESULT 9
 AAD21998
 ID AAD21998 standard; cDNA; 1248 BP.
 XX AAD21998;
 DT 12-FEB-2002 (first entry)
 XX Human transporters and ion channels (TRICH)-6 cDNA.
 XX Human; transporter and ion channel; TRICH; akinesia; cystic fibrosis;
 KW diabetes mellitus; Parkinson's disease; myasthenia gravis; dementia;
 KW

cardiac disorder; angina, hypertension; myocarditis; hyperglycaemia;
 neurological disorder; Alzheimer's disease; cataract; infertility;
 Wilson's disease; schizophrenia; Grave's disease; addison's disease;
 Huntington's disease; multiple sclerosis; meningitis; hypotensive;
 cardiac; nootropic; neuroprotective; neuroleptic; ophthalmological;
 antithyroid; anticonvulsant; goitre; antiinflammatory; ss.

Homo sapiens.

[illegible]

CDS 1. .1125

```
/*tag=
```

/product= "Human transporters and ion channels (TRICH) -6"

amidad_6tra

mat peptide

/*tag=

/product:

(TRICH) -6"

WO200177174-A2.

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
84

18-OCT-2001.

[illegible]

06-APR-2001; 2001WU-US011206.

06-APR-2000; 2000US-0195595P.

12-APR-2000; 2000US-0196872P.

20-APR-2000; 2000US-0199020P.

28-APR-2000; 2000US-0200552P.
05-MAY-2000: 2000US-0202348P

05-MAY-2000, 2000US-0202348F;
11-MAY-2000: 2000US-0203495P;

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
84

(INCY-) INCYTE GENOMICS INC.

100

Reddy K, Thornton M, Borows
Gandhi AP Vao MG Sanjanwa

Yue H, Seilhamer JJ, Walla

Lu Y, Greene BD, Raumann BE

XX
DR WPI; 2002-017448/02.
DR P-PSDB; AAE13279.
XX
XX Polypeptides of human transporters and ion channels, useful for
PT diagnosing, treating or preventing disorders of transport, neurological,
PT muscle, immunological and cell proliferative disorders.

Claim 5: Page 142-143: 150pp: English.

xx The invention relates to human transporters and ion channels (TRICH) and
 CC the polynucleotides encoding them. The composition comprising TRICH or
 CC agonist of TRICH is useful for treating a disease or condition associated
 CC with decreased expression of functional TRICH or condition associated
 CC with overexpression of TRICH respectively. The composition comprising Ab
 CC is useful for diagnosing a condition of disease associated with
 CC expression of TRICH in a subject, where the disorders include a transport
 CC disorder such as akinesia, cystic fibrosis, diabetes mellitus,
 CC Parkinson's disease, myasthenia gravis, cardiac disorders associated with
 CC transport e.g. angina, hypertension, myocarditis, neurological disorders
 CC associated with transport e.g. Alzheimer's disease, Wilson's disease,
 CC schizophrenia, cataracts, infertility, hyperglycaemia, Grave's disease,
 CC goitre, Addison's disease, Huntington's disease, dementia, multiple
 CC sclerosis, bacterial and viral meningitis. TRICH DNA is useful for
 CC generating a transcript image of a tissue or cell type, which represents
 CC the global pattern of gene expression by a particular tissue or cell type
 CC and for analysing the proteome of a tissue or cell type. TRICH DNA is
 CC used in gene therapy. The present sequence is human TRICH6
 CC

Sequence 1248 BP; 251 A; 381 C; 356 G; 260 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2.21e-107	Length:	1248
------------	-----------	---------	------

Score:	1100.00	Matches:	229
--------	---------	----------	-----

```
Db 889 TGCTCTCCACCTGCTACCGTCCGAGGAC-----TATGGCGCGCGCTCGGTGGCA 939
Qy 341 ProArgAspLeuSerThrSerAspThrCysValGluHisSerHisSer----- 356
Db 940 CCGCAGAACTCCTTCAGCGCAAGCTTGCCCGCCACACTTCCACTCCATCTCTTACAAG 999
Qy 357 -----SerProGlyGlyGlyGlyArgTyrSerAspThrProSerHisProCys 372
Db 1000 ATCGAGGAGATCTCACCAAGC-----ACA 1023
Qy 373 LeuCysSerGlyThrGlnArgSerAlaIleSerSerValSerThrGlyLeuHisSerLeu 392
Db 1024 TTAATAAACACGCTCTTCCCATGCCCTATTAGCTCCATCTCTCTGGGTTACACAGCTTT 1083
Qy 393 AlaAlaPheArgGlyLeuMetLysArgSerSerVal 405
Db 1084 ACCGACCACGAGGCTGATGAAACGCCGGAAGTCCGTT 1122
RESULT 10
AAD36247
ID AAD36247 standard; cdna; 1262 BP.
XX
XX AAD36247;
AC
XX 21-AUG-2002 (first entry)
DT
XX Human TWIK-9 cDNA.
DE
XX Human; tandem of P domains in a weak inward rectifying potassium channel;
KW TWIK-9; 56115 protein; central nervous system disorder; sleep disorder;
KW Alzheimer's disease; Parkinson's disease;
KW autonomic function disorder Huntington's disease; hypertension;
KW neuropsychiatric disorder depression; schizophrenia;
KW bipolar affective disorder; cardiac-related disorder; learning disorder;
KW cellular proliferation disorder; migration disorder;
KW myocardial infarction; memory disorder; arteriosclerosis; gene therapy;
KW amnesia; pain disorder; cancer; prophylaxis; gene; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH 5'UTR 1. .14
FT /*tag= a
FT 15. .1139
FT /*tag= b
FT /*product= "Human TWIK-9 protein"
FT /*note= "This region is specifically claimed in claim 1 as
FT SEQ ID NO:3"
FT sig_peptide 15. .86
FT /*tag= c
FT mat_peptide 87. .1136
FT /*tag= d
FT /*product= "Mature human TWIK-9 protein"
FT 3'UTR 1140. .1262
FT /*tag= e
XX
XX WO200226983-A2.
XX
XX 04-APR-2002.
XX
XX 25-SEP-2001; 2001WO-US030048.
XX
XX 25-SEP-2000; 2000US-0235059P.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Curtis RAJ;
XX
XX WPI; 2002-416481/44.
XX
XX P-PSDB; AAE22989.
XX
XX New isolated human tandem of P domains in weak inward rectifying
XX potassium channel polypeptide, 56115, useful for treating central nervous
```

```
PT system, cardiovascular, pain, and cellular proliferation disorders.
XX Claim 1; Fig 1; 9pp; English.
XX
CC The invention relates to human tandem of P domains in a weak inward
CC rectifying potassium channel polypeptides (TWIK-9) termed 56115 and
CC nucleic acid molecules encoding such polypeptides. Sequences of the
CC invention are useful for treating TWIK-9-associated or related disorders
CC such as central nervous system disorders (e.g. Alzheimer's disease,
CC Parkinson's disease, Huntington's disease), autonomic function disorders
CC (e.g., hypertension, sleep disorders, neuropsychiatric disorders (e.g.
CC depression, schizophrenia), learning or memory disorders (e.g. amnesia),
CC bipolar affective disorders, cardiac-related disorders (e.g.
CC arteriosclerosis, myocardial infarction), pain disorders, cellular
CC proliferation, growth, differentiation or migration disorders (e.g.
CC cancer) and disorders of tissues in which TWIK-9 protein is predominantly
CC expressed. They are also useful in screening assays, detection assays
CC (e.g. chromosomal mapping, tissue typing, forensic biology), predictive
CC medicine (e.g., diagnostic assays, prognostic assays, monitoring clinical
CC trials and pharmacogenomics) and in methods of treatment (e.g.
CC therapeutic and prophylactic). TWIK-9 polynucleotides are used in gene
CC therapy. The present sequence is human TWIK-9 cDNA
XX
```

SQ Sequence 1262 BP; 251 A; 387 C; 361 G; 263 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2 25e-107 Length: 1262
Score: 1100.00 Matches: 229
Percent Similarity: 67.07% Conservative: 48
Best Local Similarity: 55.45% Mismatches: 86
Query Match: 52.26% Indels: 50
DB: 6 Gaps: 5

US-09-939-483-5 (1-405) x AAD36247 (1-1262)

```
Qy 1 GluAsnValArgThrLeuAlaLeuIleValCysThrPheThrTyrLeuLeuValGlyAla 20
Db 24 CAGAAGCTGGGACTCTGCTCCCTCATGCTCTGCACCTTACCTTACCTGTGTGGTGGCGCC 83
Qy 21 AlaValPheAspAlaLeuGluSerGluProGluMetIleGluArgGlnArgLeuGluLeu 40
Db 84 GCCGTGTTCCAGCGCCTCGAGTCGGACACGAGATCGCGGAGGAGAACTCAAGGCC 143
Qy 41 ArgGlnLeuGluLeuArgAlaArgTyrAsnLeuSerGluGlyTyrGluGluLeuGlu 60
Db 144 GAGGAGATCCGGATCAAGGGGAGTACACATCAGCAGCGAGGACTACCGCGAGCTGGAG 203
Qy 61 ArgValValLeuArgLeuLysProHisLysAlaGlyValGlnTrpArgPheAlaGlySer 80
Db 204 CTGGTGATCTGCAGTCGGAACCGCACCGCGCGGTCCAGTGGAAATTCGCGCGCTCC 263
Qy 81 PheTyrPheAlaIleThrValIleThrThrIleGlyTyrGlyHisAlaAlaProSerThr 100
Db 264 TTCTACTTTCGATCAGGTTCATCACCACATAGGTTATGGGCACCTGCACCTGGCACC 323
Qy 101 AspGlyGlyLysValPheCysMetPheTyrAlaLeuLeuGlyIleProLeuThrLeuIle 120
Db 324 GATCGGGCAAGGCCCTTCTGCATGTTCTACGCGCTGCTGGCATCCCGCTGACACTGGTC 383
Qy 121 MetPheGlnSerLeuGlyGluArgIleAsnThrPheValArgTyrLeuLeuHisArgAla 140
Db 384 ATGTTTTCAGAGCCTGGCGGCGCATGAACACCTTCCTGCGCTTACCTGTCTGAAGCGCAT 443
Qy 141 LysArgGlyLeuGlyMetArgHisAlaGluValSerMetAlaAsnMetValLeuIleGly 160
Db 444 AAGAAGTGTGTGGCATGCGCAACACTGACGTGCTATGAGAACATGGTACTGTGGGC 503
Qy 161 PheValSerCysIleSerThrLeuCysIleGlyAlaAlaPheSerTyrTyrGluArg 180
Db 504 TTCTTCTCTGCATGGGACGCTGTGCATCGGGCGCGCCTTCTCCAGTGTGAGGAG 563
Qy 181 TrpThrPhePheGlnAlaTyrTyrCysPheIleThrLeuThrThrIleGlyPheGly 200
```



```
Db 564 TGGAGCTTCTCCAGCCCTACTACTACTGCTTCATCAGTTGACTTACCATTTGGGTTGGG 623
Qy 201 AspTyrValAlaLeuGlnLysAspGlnAlaLeuGlnThrGlnProGlnTyrValAlaPhe 220
Db 624 GACTACGTGGCCCTGTCAGACCAAGGGCCCTCCAGAGAAGCCGCTCTACGTGGCCTTT 683
Qy 221 SerPheValTyrIleLeuThrGlyLeuThrValIleGlyAlaPheLeuAsnLeuValVal 240
Db 684 AGCTTTATGATATCCTGGTGGGGCTGACGGTCAATCGGGGCTTCCTCAACCTGGTCGT 743
Qy 241 LeuArgPheMetThrMetAsnAlaGluAspGlnLysArgAspAlaGluHisArgAlaLeu 260
Db 744 CTCAGTTCTTGACCATGACATGACGATGAGCGCGGATGCTGAGAGAGAGGCATCC 803
Qy 261 LeuThrHisAenGlyGlnAlaValGlyLeuGlyGlyLeuSerCysLeuSerGlySerLeu 280
Db 804 CTCGCGGAAACCGCAAC-----AGCATGGTCATTTCACATCCCT 842
Qy 281 GlyAspValArgProArgAspProValThrCysAlaAlaAlaGlyValGlyVal 300
Db 843 GAGGAGCGCGCGCCAGCGGCC----- 866
Qy 301 GlyValGlyGlySerGlyPheArgAsnValTyrAlaGluValLeuHisPheGlnSerMet 320
Db 867 -----AGGTACAGGGGAGCTCCGGACCTCCATCTCTGTG 902
Qy 321 CysSerCysLeuTyrTyrLysSerArgGlnLysLeuGlnTyrSerIleProMetIleIle 340
Db 903 TGCTCTGCACCTGCTACCGCTCGCAGGAC-----TATGGCGGCGCTCGGTGGCA 953
Qy 341 ProArgPheLeuSerThrSerAspThrCysValGluHisSerHisSer----- 356
Db 954 CCGCAGAACTCTTCAGCGCAAGCTTGCCCGCCCACTACTTCCACTCTCTTACAAG 1013
Qy 357 -----SerProGlyGlyGlyArgTyrSerAspThrProSerHisProCys 372
Db 1014 ATCAGGAGATCTCACAGC-----ACA 1037
Qy 373 LeuCysSerGlyThrGlnArgSerAlaIleSerValSerThrGlyLeuHisSerLeu 392
Db 1038 TTAATAAACACGCTCTTCCCATCGCTATTAGCTCCATCTCTCTGGGTTACACAGCTTT 1097
Qy 393 AlaAlaPheArgGlyLeuMetLysArgArgSerSerVal 405
Db 1098 ACCGACCACACAGAGGCTGATGAACGCGGAAGTCCGTT 1136
RESULT 11
ID ADI27947 standard; cDNA; 1262 BP.
XX AC ADI27947;
XX DT 06-MAY-2004 (first entry)
XX DE Human TWIK-9 cDNA.
XX Human; TWIK-9; gene; ss; ion channel family; ICF; cancer; leukaemia;
KW Alzheimer's disease; Parkinson's disease; multiple sclerosis; epilepsy;
KW hepatic disorder; cardiovascular disorder; cytostatic; neuroprotective;
KW nontropic; antiparkinsonian; hepatotropic; cardiovascular.
XX OS Homo sapiens.
XX PN US2003165891-A1.
XX PD 04-SEP-2003.
XX PF 15-MAY-2002; 2002US-00146733.
XX PR 29-FEB-2000; 2000US-00515520.
XX PR 29-FEB-2000; 2000US-0185938P.
XX PR 03-MAR-2000; 2000US-00518866.
XX PR 07-APR-2000; 2000US-0195734P.
```

```
PR 11-APR-2000; 2000US-0195993P.
PR 26-APR-2000; 2000US-0199799P.
PR 19-SEP-2000; 2000US-0233537P.
PR 25-SEP-2000; 2000US-0235018P.
PR 25-SEP-2000; 2000US-0235059P.
PR 15-DEC-2000; 2000US-0256240P.
PR 18-DEC-2000; 2000US-0256588P.
PR 21-DEC-2000; 2000US-0258028P.
PR 28-FEB-2001; 2001US-00796720.
PR 06-APR-2001; 2001US-00828035.
PR 11-APR-2001; 2001US-00833081.
PR 25-APR-2001; 2001US-00843128.
PR 19-SEP-2001; 2001US-00957683.
PR 25-SEP-2001; 2001US-00964252.
PR 25-SEP-2001; 2001US-00964256.
PR 17-DEC-2001; 2001US-00024623.
XX (MILL-) MILLENNIUM PHARM INC.
XX Curtis RAJ, Gluckemann MA, Silos-Santiago I;
XX WPI; 2004-069000/07.
XX P-PSDB; ADI27948.
XX TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9,
XX alpha-delta-4, 54414, or 53763 nucleic acids and proteins, useful for
XX preventing, diagnosing and treating e.g. cancers, Alzheimer's disease and
XX cardiovascular disorders.
XX Claim 1; SEQ ID NO 40; 638pp; English.
XX The invention relates to TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611,
XX IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and 53763 ion channel
XX family (ICF) nucleic acids and proteins. The TWIK-6, TWIK-7, IC23927,
XX TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and
XX 53763 ICF nucleic acids and proteins may be used for preventing,
XX diagnosing and treating ICF-related diseases. The sequences may be used
XX to treat disorders associated with decreased expression by rectifying
XX mutations or deletions in a patient's genome that affect the activity of
XX ICF proteins by expressing inactive proteins or to supplement the
XX patients own production of ICF proteins. The proteins may also be used as
XX antigens in the production of antibodies against ICF proteins and in
XX assays to identify modulators of ICF protein expression and activity. The
XX anti-ICF protein antibodies, agonists and antagonists may be used to
XX regulate ICF protein expression and activity. The antibodies may also be
XX used as diagnostic agents for detecting the presence of ICF proteins in
XX samples (e.g. by immunoassay). The nucleic acids and proteins may be used
XX to prevent, diagnose and treat a wide variety of disorders, e.g. cancers
XX and leukaemia, Alzheimer's disease, Parkinson's disease, multiple
XX sclerosis, epilepsy, hepatic disorders and cardiovascular disorders. This
XX sequence represents cDNA encoding the human TWIK-9 protein of the
XX invention. Note: The sequence data for this patent is also available in
XX electronic format from USPTO at seqdata.uspto.gov/sequence.html.
XX Sequence 1262 BP; 251 A; 387 C; 361 G; 263 T; 0 U; 0 Other;
SQ
```

```
Alignment Scores:
Pred. No.: 2,25e-107 Length: 1262
Score: 1100.00 Matches: 229
Percent Similarity: 67.07% Conservatives: 48
Best Local Similarity: 55.45% Mismatches: 86
Query Match: 52.26% Indels: 50
DB: 12 Gaps: 5
```

US-09-939-483-5 (1-405) x ADI27947 (1-1262)

```
Qy 1 GluAsnValArgThrLeuAlaLeuIleValCysThrPheThrTyrLeuLeuValGlyAla 20
Db 24 CAGAACGTGGCGGACTCTGTCCCTCATGCTGCACCTTACCTGCTGGTGGGGGCC 83
Qy 21 AlaValPheAspAlaLeuGluSerGluProGluMetIleGluArgGlnArgLeuGluLeu 40
Db 84 GCCGTGTTCCAGCCCTTCGAGTCGACACGATGCGCGAGGAGGAACTCAAAGCC 143
```

```
QY 41 ArgGlnLeuGluLeuArgAlaArgTyrAsnLeuSerGluGlyGlyTyrGluGluLeuGlu 60
Db 144 GAGGAGATCCGGATCAGGGAAGTACAAATCAGCAGCAGGAGTACCGGAGCTGGAG 203

QY 61 ArgValValLeuArgLeuLysProHisLysAlaGlyValGlnTyrArgPheAlaGlySer 80
Db 204 CTGGTGATCTCGCAGTCGGAACCGCAGCGCGCGCTCCAGTGGAAATTCGCGGGCTCC 263

QY 81 PheTyrPheAlaIleThrValIleThrIleGlyTyrGlyHisAlaAlaProSerThr 100
Db 264 TTCTACTTTTGGCATCAGGTCATCACCACCATGGTTATGGGCACGCTGCACCTGGCACC 323

QY 101 AspGlyGlyLysValPheCysMetPheTyrAlaLeuLeuGlyIleProLeuThrLeuIle 120
Db 324 GATCGGGCAAGCGCTTCTGCATGTTCTACGCGCTGTGGCATCCGCTGACACTGGTC 393

QY 121 MetPheGlnSerLeuGlyGluArgIleAsnThrPheValArgTyrLeuLeuHisArgAla 140
Db 384 ATGTTTCAGAGCTTGGCGGAGCGCATGAACACCTTCTCGCGCTACCTGCTGAAGCGCAT 443

QY 141 LysArgGlyLeuGlyMetArgHisAlaGluValSerMetAlaAsnMetValLeuIleGly 160
Db 444 AAGAGTGTGTGTCATCGCACTGCGAACAACACTGATGTCATGGAGAACATGGTGCTGGGC 503

QY 161 PheValSerCysIleSerThrLeuCysIleGlyAlaAlaAlaPheSerTyrTyrGluArg 180
Db 504 TTCTTCTCTGATGGGAGCGCTGTGTCATCGGGCGCGCGCTTCTCCAGTGTGAGGAG 563

QY 181 TrpThrPheGlnAlaTyrTyrCysPheIleThrLeuThrIleGlyPheGly 200
Db 564 TGGAGCTTCTTCCACGCTACTACTACTGCTTATCATCAGTTGACTACCATTTGGGTCGGG 623

QY 201 AspTyrValAlaLeuGlnLysAspGlnAlaLeuGlnThrGlnProGlnTyrValAlaPhe 220
Db 624 GACTACGTGGCCCTGCGAGCAAGGGCGCGCTGCGAAGAAGCGCTCTACGTGGCGCTTT 683

QY 221 SerPheValTyrIleLeuThrGlyLeuThrValIleGlyAlaPheLeuAsnLeuValVal 240
Db 684 AGCTTTATGATATCTCTGTTGGGCTGACGTCATCGGGCGCTTCTCAACCTGGTCTGTC 743

QY 241 LeuArgPheMetThrMetAsnAlaGluAspGluLysArgAspAlaGluHisArgAlaLeu 260
Db 744 CTCAGGTTCTTGACATGAACATGAGATGAGGATGAGCGGGATGCTGAAGAGGCGCATCC 803

QY 261 LeuThrHisAsnGlyGlnAlaValGlyLeuSerCysLeuSerGlySerLeu 280
Db 804 CTGCGCGAAACCGCAAC-----AGCATGGTTCATTCATCCCT 842

QY 281 GlyAspValArgProArgAspProValThrCysAlaAlaAlaGlyGlyValGlyVal 300
Db 843 GAGGAGCGCGCGCCAGCGCGCC-----866

QY 301 GlyValGlyGlySerGlyPheArgAsnValTyrAlaGluValLeuHisPheGlnSerMet 320
Db 867 -----AGGTACAAGCGCGAGCTCCCGGACCTGCGAGTCTGTG 902

QY 321 CysSerCysLeuTrpTyrLysSerArgGluLysLeuGlnTyrSerIleProMetIleIle 340
Db 903 TGCTCTCGACCTGCTACCCCTCGAGGAC-----TATGGCGCGCGCTCGGTGGCA 953

QY 341 ProArgAspLeuSerThrSerAspThrCysValGluHisSerHisSer-----356
Db 954 CCGCAGAACTCTTCAGCGCCCAAGCTTGGCCCACTACTTCCACTCCATCTCTTACAG 1013

QY 357 -----SerProGlyGlyGlyArgTyrSerAspThrProSerHisProCys 372
Db 1014 ATCAGGAGATCTCACCAAGC-----ACA 1037

QY 373 LeuCysSerGlyThrGlnArgSerAlaIleSerValSerThrGlyLeuHisSerLeu 392
Db 1038 TTAAAAAAGAGCTCTTCCCATCGCTATTAGTCTCACTCTCTCTGCGGTACAGCTTT 1097
```

```
QY 393 AlaAlaPheArgGlyLeuMetLysArgArgSerSerVal 405
Db 1098 ACCGACCACCAGAGGCTGATGAACCGCGGAGCTCGTT 1136

RESULT 12
AAAY5887
ID AAA75887 standard; cDNA; 1441 BP.
XX
AC AAA75887;
XX
DT 22-JAN-2001 (first entry)
XX
DE Expressed sequence tag (EST) related to a human KCNN1 cDNA.
XX
KW Human; KCNN1: potassium channel; cancer; pulmonary disease; depression;
cardiovascular disease; inflammatory disease; renal disease; pain;
psychiatric disorder; schizophrenia; neurodegenerative disease;
Alzheimer's disease; neurological disorder; migraine; epilepsy;
sleep-related disorder; erectile dysfunction; alopecia;
expressed sequence tag; EST; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 65..1189
FT FT /*tag= a
XX
PN WO200053628-A2.
XX
PD 14-SEP-2000.
XX
PF 02-MAR-2000; 2000WO-EP001750.
XX
PR 05-MAR-1999; 99GB-00005061.
PR 10-FEB-2000; 2000GB-00003112.
XX
PA (SMIK ) SMITHLINE BEECHAM PLC.
XX
PI Duckworth DM, Godden RJ, Chapman CG, Meadows HJ;
XX
DR WPI; 2000-587424/55.
DR P-PSDB; AAB18813.
XX
PT Polypeptides and polynucleotides of the potassium channel family, useful
for identifying agonists/antagonists of therapeutic use and diagnosis and
treatment of cancer, pulmonary, cardiovascular, inflammatory and renal
disease.
XX
PS Claim 11; Page 25-26; 36pp; English.
XX
The present sequence represents an expressed sequence tag (EST) which is
related to a cDNA encoding a human KCNN1 polypeptide. The polypeptide is
a member of the potassium channel family. The KCNN1 polypeptides and
polynucleotides are useful for treating diseases including cancer,
pulmonary, cardiovascular, inflammatory or renal diseases, pain,
psychiatric disorders including depression and schizophrenia,
neurodegenerative disease including Alzheimer's, neurological disorders,
migraine, epilepsy, sleep-related disorders, erectile dysfunction and
alopecia. KCNN1 polynucleotides are useful as diagnostic reagents for
detecting mutations in the associated gene
XX
SQ Sequence 1441 BP; 287 A; 436 C; 389 G; 328 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.: 2,75e-107 Length: 1441
Score: 1100.00 Matches: 229
Percent Similarity: 67.07% Conservative: 48
Best Local Similarity: 55.45% Mismatches: 86
Query Match: 52.26% Indels: 50
DB: 3 Gaps: 5

US-09-939-483-5 (1-405) x AAAY5887 (1-1441)
```

Qy 1 GluAsnValArgThrLeuAlaLeuIleValCysThrPheThrTyrLeuLeuValGlyAla 20
Db :::
74 CAGAACGGCGAGACTGTCTCCCTCATCGTGCACCTTCACCTACCTGTGGTGGCGCC 133
Qy 21 AlaValPheAspAlaLeuGluSerGluProGluMetIleGluArgGlnArgLeuGluLeu 40
Db :::
134 GCGGTGTTGACGCGCTCGACTCGGACACAGAGATCGCGAGGAGAGAACTCAAGCC 193
Qy 41 ArgGlnLeuGluLeuArgAlaArgTyrAsnLeuSerGluGlyGlyTyrGluGluLeuGlu 60
Db :::
194 GAGGAGATCCGGATCAAGGGAAGTACAAATCATCAGCAGCGAGGACTACCGGACGTGGAG 253
Qy 61 ArgValValLeuArgLeuLysProHisLysAlaGlyValGlnTyrArgPheAlaGlySer 80
Db :::
254 CTGTGTATCTGCGATCGAAGCCGACCGCGCGGCTCCAGTGGAAATTCGCCGGCTCC 313
Qy 81 PheTyrPheAlaIleThrValIleThrThrIleGlyTyrGlyHisAlaAlaProSerThr 100
Db :::
314 TTCTTACITTCGATCAGGTCATCACCACCATAGTATTATGGCAGCGCTGCACCTGGCACC 373
Qy 101 AspGlyGlyLysValPheCysMetPheTyrAlaLeuLeuGlyIleProLeuThrLeuIle 120
Db :::
374 GATCGGCGCAAGGCTTCTGCATGTTCTACCGCGTGTGGCATCCCGCTGACACTGGTC 433
Qy 121 MetPheGlnSerLeuGlyGluArgIleAsnThrPheValArgTyrLeuLeuHisArgAla 140
Db :::
434 ATGTTCCAGAGCCCTGGGCGAGCGGATGAACACCTTCGTGGCGCTACCTGCTGAAGCGGATT 493
Qy 141 LysArgGlyLeuGlyMetArgHisAlaGluValSerMetAlaAsnMetValLeuIleGly 160
Db :::
494 AAGAGTGCTGTGCATGCGCAACACTGACGTGTTCTATGGAGAACATGGTGACTGTGGC 553
Qy 161 PheValSerCysIleSerThrLeuCysIleGlyAlaAlaAlaPheSerTyrTyrGluArg 180
Db :::
554 TTCTTCTCTCATGCGGACGCTGTGCATCGGCGCGGCTTCTCCAGTGTGAGGAG 613
Qy 181 TrpThrPhePheGlnAlaTyrTyrCysPheIleThrLeuThrIleGlyPheGly 200
Db :::
614 TGGAGCTTCTTCCAGCGCTACTACTGCTTCTATCATCAGTTGACTACCATTTGGGTTCCGG 673
Qy 201 AspTyrValAlaLeuGlnLysAspGlnAlaLeuGlnThrGlnProGlnTyrValAlaPhe 220
Db :::
674 GACTACGTGGCCCTGCAGACCAAGGGCGCTTCAGAAAGCGCGCTACGTGGCCTTT 733
Qy 221 SerPheValTyrIleLeuThrGlyLeuThrValIleGlyAlaPheLeuAsnLeuValVal 240
Db :::
734 AGCTTTATGTATCTGTGTGGGCTGACGTGCTCATCGGGCGCTTCTCAACTGTCGTC 793
Qy 241 LeuArgPheMetThrMetAsnAlaGluAspGluLysArgAspAlaGluHisArgAlaLeu 260
Db :::
794 CTCAGGTTCTTGACCATGAACAGTGAAGATGAGCGGGGATGCTGAAGAGAGGCGCATCC 853
Qy 261 LeuThrHisAsnGlyGlnAlaValGlyLeuGlyGlyLeuSerCysLeuSerGlySerLeu 280
Db :::
854 CTCGCGGAACCGCAAC-----AGCATGGTCATTTCACATCCCT 892
Qy 281 GlyAspValArgProArgAspProValThrCysAlaAlaAlaGlyValGlyVal 300
Db :::
893 GAGGAGCGCGCGCCAGCGCGCC----- 916
Qy 301 GlyValGlyGlySerGlyPheArgAsnValTyrAlaGluValLeuHisPheGlnSerMet 320
Db :::
917 -----AGGTACAAGCGGACGTCGCGGACCTGTCAGCTGTGT 952
Qy 321 CysSerCysLeuTyrTyrLysSerArgGluLysLeuGlnTyrSerIleProMetIleIle 340
Db :::
953 TGCTCTGCACCTGCTACCGCTCGCAGGAC-----TATGGCGCGCGCTCGTGCA 1003
Qy 341 ProArgAspLeuSerThrSerAspThrCysValGluHisSerHisSer----- 356
Db :::
1004 CCGCAGAACTCTTCAGCGCCCAAGCTTCCCGCCCACTACTTCCACTCCATCTCTTACAAG 1063
Qy 357 -----SerProGlyGlyGlyArgTyrSerAspThrProSerHisProCys 372

Db 1064 ATCAGAGAGATCTCACCAAGC-----ACA 1087
Qy 373 LeuCysSerGlyThrGlnArgSerAlaIleSerSerValSerThrGlyLeuHisSerLeu 392
Db :::
1088 TTAATAAACAGCTCTTCCCATCGCTTATAGCTCCATCTCTCTGGGTTACACAGCTTT 1147
Qy 393 AlaAlaPheArgGlyLeuMetLysArgArgSerVal 405
Db :::
1148 ACCGACCACAGAGGCTGATGAACACGCCGGAAGTCCGTT 1186
RESULT 13
AAH75002
ID AAH75002 standard; cDNA; 2312 BP.
XX
AC AAH75002;
XX
DT 29-OCT-2001 (first entry)
XX
DE cDNA sequence of human potassium channel protein KCNB.
XX Human; potassium channel protein; KCNB; breast tissue; cancer; stroke;
XX potassium channel-associated disorder; brain associated disorder;
XX epilepsy; Alzheimer's disease; Parkinson's disease; multiple sclerosis;
XX migraine; psychiatric disorder; depression; schizophrenia; diabetes;
XX bipolar disease; heart disease; arrhythmia; pancreas disease;
XX pancreatitis; ss.
XX Homo sapiens.
XX
XX W0200166741-A2.
XX
PD 13-SEP-2001.
XX
XX 02-MAR-2001; 2001WO-US006801.
XX
PR 03-MAR-2000; 2000US-0186915P.
XX
XX (TULA-) TULARIK INC.
XX
XX Mu D, Powers S;
XX
XX WPI; 2001-522949/57.
XX
PT A nucleic acid encoding a potassium channel, termed KCNB (potassium channel expressed in breast), useful in the diagnosis, prognosis or treatment of diseases associated with altered KCNB activity or expression, e.g. cancer and diabetes.
XX
PS Claim 6; Page 80-81; 82pp; English.
XX
XX The present sequence encodes a human potassium channel protein, termed KCNB. KCNB is expressed in breast tissue. The KCNB polypeptides are useful for identifying a compound that modulates its activity. The KCNB polypeptide and nucleic acid are useful for detecting cancer cells in biological samples. The inhibitor of the potassium channel polypeptide is useful for inhibiting proliferation of a cancer cell and for treating a potassium channel-associated disorder. The KCNB nucleic acids, proteins, and/or antibodies are useful in the diagnosis or prognosis, or treatment of diseases associated with altered KCNB activity or expression. Such diseases are cancer, brain associated disorders (such as epilepsy, Alzheimer's disease, Parkinson's disease, stroke, multiple sclerosis, CC migraine), psychiatric disorders (such as depression, schizophrenia, bipolar diseases) and diseases related to the heart (such as CC arrhythmias), diseases related to pancreas (such as pancreatitis and CC diabetes)
XX
SQ Sequence 2312 BP; 542 A; 627 C; 548 G; 595 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 5,65e-107 Length: 2312
Score: 1100.00 Matches: 229
Percent Similarity: 67.07% Conservative: 48

Best Local Similarity:	55.45%	Mismatches:	86
Query Match:	52.26%	Indels:	50
DB:	5	Gaps:	5

US-09-939-483-5 (1-405) x AAH75002 (1-2312)

Qy	1	Glua	Val	Arg	Thr	Leu	Ala	Leu	Val	Cys	Thr	Ph	Thr	Thr	Leu	Leu	Val	Gly	Ala	20	
Db	50	CAGA	CGT	CGG	ACT	CTG	TCC	CTC	AT	CGT	CTG	CA	CTT	CG	ACT	TAC	CTG	TGG	CGCC	109	
Qy	21	Ala	Val	Phe	Asp	Ala	Leu	Glu	Ser	Glu	P	ro	Glu	Met	Ile	Glu	A	rg	Gln	Leu	40
Db	110	GCG	TGT	TGA	CGCC	CTC	AGT	TCG	GAC	CA	CGC	AG	AT	CGC	GAG	AGG	AGG	AA	CT	CAA	169
Qy	41	Arg	Gln	Leu	Glu	Leu	Ala	Arg	Tyr	Asn	Leu	Ser	Glu	Gly	Gly	Tyr	Glu	Leu	Glu	Leu	60
Db	170	GAG	GAG	AT	CGG	AT	CA	AGG	GA	G	TAC	AA	CA	T	CA	G	AC	G	AG	CA	229
Qy	61	Arg	Val	Val	Leu	Arg	Leu	Leu	ys	P	ro	His	Ala	Gly	Val	Gln	T	Pr	A	rg	80
Db	230	CTG	GT	AT	CT	CT	CA	G	T	CG	CA	CG	CG	CG	CG	CG	T	CG	AG	T	289
Qy	81	Phe	Tyr	Phe	Ala	Ile	Thr	Val	Ile	Thr	Thr	Ile	Gly	Tyr	Gly	His	Ala	Ala	P	ro	100
Db	290	TTC	T	ACT	TTT	G	CA	T	CA	G	GT	CA	T	CA	CC	AT	AG	TT	AT	G	349
Qy	101	Asp	Gly	Gly	ys	Val	Phe	Cys	Met	Phe	Tyr	Ala	Leu	Leu	Gly	Ile	Pro	Leu	Thr	Leu	120
Db	350	GAT	CG	GG	CA	AG	CC	CTT	CT	CA	G	CG	TG	CT	G	GC	AT	CC	CG	T	409
Qy	121	Met	Phe	Gln	Ser	Leu	Gly	C	lu	Arg	Ile	Asn	Thr	Phe	Val	Arg	Tyr	Leu	Leu	His	140
Db	410	ATG	TT	CC	AG	CG	CT	G	G	CG	AG	CA	CA	CTT	TC	G	T	CG	CT	T	469
Qy	141	Lys	Arg	Gly	Leu	Gly	Met	Arg	His	Ala	Glu	Val	Ser	Met	Ala	Asn	Met	Val	Leu	Ile	160
Db	470	AAG	AA	G	T	GT	G	CA	T	GC	CA	CA	CT	CA	CG	T	GT	CT	AT	G	529
Qy	161	Phe	Val	Ser	Cys	Ile	Ser	Thr	Leu	Cys	Ile	Gly	Ala	Ala	Ala	Phe	Ser	Tyr	Tyr	Glu	180
Db	530	TTT	CT	CT	CT	CG	AT	G	GG	CA	CG	T	CG	CG	CG	CG	CG	CTT	CT	C	589
Qy	181	Trp	Thr	Phe	Phe	Gln	Ala	Tyr	Tyr	Tyr	Cys	Phe	Ile	Thr	Leu	Thr	Thr	Ile	Gly	Phe	200
Db	590	TGG	AG	CT	T	CTT	CA	G	CC	T	ACT	T	ACT	T	GC	T	CA	T	CA	G	649
Qy	201	Asp	Tyr	Val	Ala	Leu	Gln	lys	Asp	Gln	Ala	Leu	Gln	Thr	Gln	Pro	Gln	Tyr	Val	Ala	220
Db	650	GAC	T	AG	T	GG	CC	CT	GC	AG	CA	AA	G	GG	CG	CG	CT	CT	CA	G	709
Qy	221	Ser	Phe	Val	Tyr	Ile	Leu	Thr	Gly	Leu	Thr	Val	Ile	Gly	Ala	Phe	Leu	Asn	Leu	Val	240
Db	710	AGC	TTT	AT	AT	AT	CT	CG	T	GG	GG	GT	CA	CG	GT	CA	T	CG	GG	CG	769
Qy	241	Leu	A	cp	Phe	Met	Thr	Met	Asn	Ala	Glu	Asp	Glu	lys	Arg	Phe	Ala	Glu	His	Arg	260
Db	770	CTC	AG	GT	T	CTT	G	AC	CA	T	GA	CA	G	T	G	AG	CG	CG	CG	AT	829
Qy	261	Leu	Thr	His	Asn	Gly	Gln	Ala	Val	Gly	Leu	Gly	Leu	Ser	Cys	Leu	Ser	Gly	Ser	Leu	280
Db	830	CT	C	CG	CG	GA	AA	C	CG	CA	AC	-----	-----	-----	-----	-----	-----	-----	-----	868	
Qy	281	Gly	Asp	Val	Arg	Pro	Arg	Asp	Pro	Val	Thr	Cys									

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 16, 2005, 02:46:00 ; Search time 231 Seconds
(without alignments)
2868.797 Million cell updates/sec

Title: US-09-939-483-5
Perfect score: 2105
Sequence: 1 ENVRTALICTFTYLLVGA.....STGLHSLAARGLMKRRSSV 405

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-O=/cgm2_1/USPTO spool/US09939483/runat 15092005 111357 9602/app query.fasta_1.583
-DB=Issued Patents NA -OEMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOPCL=0
-LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFM=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09939483 @CGN 1 1 177 @runat 15092005 111357 9602 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEX=7

Database :

Issued Patents NA:
1: /cgm2_6/ptodata/1/ina/5A COMB.seq:
2: /cgm2_6/ptodata/1/ina/5B COMB.seq:
3: /cgm2_6/ptodata/1/ina/6A COMB.seq:
4: /cgm2_6/ptodata/1/ina/6B COMB.seq:
5: /cgm2_6/ptodata/1/ina/PCTUS COMB.seq:
6: /cgm2_6/ptodata/1/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1819	86.4	2514	3	US-09-144-914-3
2	1819	86.4	2588	4	US-09-949-016-1555
3	1378	65.5	43507	4	US-09-949-016-13297
4	1100	52.3	1167	4	US-09-949-016-1760
5	774	36.8	88758	4	US-09-949-016-13502
6	773	36.7	1227	4	US-09-362-842-11
7	631.5	30.0	601	4	US-09-949-016-60471
8	354.5	16.8	2710	4	US-09-949-016-1497
9	354.5	16.8	2730	4	US-09-799-451-432
10	354.5	16.8	2730	4	US-09-949-016-1130
11	354	16.8	1086	4	US-09-362-842-13
12	345	16.4	1994	3	US-09-236-080-5

13	341	16.2	1182	3	US-09-432-470-1	Sequence 1, Appli
14	341	16.2	1218	3	US-09-432-470-3	Sequence 3, Appli
15	341	16.2	2733	4	US-09-949-016-1938	Sequence 1938, Ap
16	341	16.2	2772	4	US-09-949-016-1042	Sequence 1042, Ap
17	341	16.2	3996	4	US-09-620-312D-195	Sequence 195, App
18	338	16.1	1246	3	US-09-236-080-1	Sequence 1, Appli
19	338	16.1	3300	3	US-09-336-643A-82	Sequence 82, Appli
20	334.5	15.9	1882	4	US-09-814-915A-45	Sequence 45, Appli
21	334.5	15.9	1894	3	US-08-749-816-1	Sequence 1, Appli
22	334.5	15.9	1894	3	US-09-144-914-1	Sequence 1, Appli
23	319.5	15.2	1497	4	US-09-561-763-3	Sequence 3, Appli
24	319.5	15.2	1497	4	US-09-431-367B-3	Sequence 3, Appli
25	319.5	15.2	3452	4	US-09-561-763-1	Sequence 1, Appli
26	319.5	15.2	3452	4	US-09-431-367B-1	Sequence 1, Appli
27	317.5	15.1	438	4	US-09-362-842-68	Sequence 68, Appli
28	317.5	15.1	438	4	US-09-270-767-56	Sequence 56, Appli
29	317.5	15.1	438	4	US-09-270-767-15338	Sequence 15338, A
30	310	14.7	2988	4	US-09-362-842-1	Sequence 1, Appli
31	298	14.2	996	4	US-09-561-763-6	Sequence 6, Appli
32	298	14.2	996	4	US-09-431-367B-6	Sequence 6, Appli
33	298	14.2	1575	4	US-09-561-763-4	Sequence 4, Appli
34	298	14.2	1575	4	US-09-431-367B-4	Sequence 4, Appli
35	292.5	13.9	2287	4	US-09-561-763-7	Sequence 7, Appli
36	292.5	13.9	2287	4	US-09-431-367B-7	Sequence 7, Appli
37	292.5	13.9	2571	3	US-09-336-643A-80	Sequence 80, Appli
38	283.5	13.5	939	4	US-09-561-763-9	Sequence 9, Appli
39	283.5	13.5	939	4	US-09-431-367B-9	Sequence 9, Appli
40	259.5	12.3	2441	1	US-08-332-312-1	Sequence 1, Appli
41	251	11.9	1011	1	US-08-332-312-3	Sequence 3, Appli
42	248.5	11.8	1203	4	US-09-561-763-12	Sequence 12, Appli
43	248.5	11.8	1203	4	US-09-431-367B-12	Sequence 12, Appli
44	248.5	11.8	1506	4	US-09-561-763-10	Sequence 10, Appli
45	248.5	11.8	1506	4	US-09-431-367B-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1
US-09-144-914-3
; Sequence 3, Application US/09144914
; Patent No. 6309855
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Fink, Michel
; APPLICANT: Lazdunski, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 989.6705CIP
; CURRENT APPLICATION NUMBER: US/09/144,914
; EARLIER FILING DATE: 1998-09-01
; EARLIER FILING DATE: 1996-11-15
; EARLIER FILING DATE: 1996-11-15
; EARLIER APPLICATION NUMBER: 60/095,234
; EARLIER FILING DATE: 1998-08-04
; EARLIER APPLICATION NUMBER: FR 96/01565
; EARLIER FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2514

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (126)..(1307)
FEATURE:
OTHER INFORMATION: TASK
US-09-144-914-3

Alignment Scores: 1,23e-220 Length: 2514
Pred. No.: 1819.00 Matches: 357
Score:

Percent Similarity:	90.37%	Conservative:	9
Best Local Similarity:	88.15%	Mismatches:	25
Query Match:	86.41%	Indels:	14
DB:	3	Gaps:	2
US-09-939-483-5 (1-405) x US-09-144-914-3 (1-2514)			
QY	1	GlusnValArgThrLeuAlaLeuIleValCysThrPheThrTyrLeuLeuValGlyAla	20
DB	135	CAGAAGTGGCGACGCTGGCGCTCATCGTGTGCACCTTCACCTACCTGCTGTTGGGCGCC	194
QY	21	AlaValPheAspAlaLeuGluSerGluProGluMetIleGluArgGlnArgLeuGluLeu	40
DB	195	GCGGTCTTCGACGCGCTGGAGTCGGAGCCGAGCTGATCGAGCGCGCTGGAGCTG	254
QY	41	ArgGlnLeuGluLeuArgAlaArgTyrAsnLeuSerGluGlyGlyTyrGluGluLeuGlu	60
DB	255	CGCAGAGAGAGCTGGCGGCGCTACAACTCAGCCAGGCGGCTTCAGAGAGCTGGAG	314
QY	61	ArgValValLeuArgLeuLysProHisLysAlaGlyValGlnTrpArgPheAlaGlySer	80
DB	315	CGCGTGTGCGCTCAAGCGCACAGGCGCGGCTGCAGTGGCGCTTCGCGGCTCC	374
QY	81	PheTyrPheAlaIleThrValIleThrThrIleGlyTyrGlyHisAlaAlaProSerThr	100
DB	375	TTCTACTTCGCCATCACCTACCACTCGGTACGGGACGCGCGCACCCAGCACG	434
QY	101	AspGlyGlyLysValPheCysMetPheTyrAlaLeuLeuGlyIleProLeuThrLeuIle	120
DB	435	GATGGCGGCAAGGTGTTCGATGTTCACGCGCTGCTGGGCATCCCGCTCACGCTCGTC	494
QY	121	MetPheGlnSerLeuGlyGluArgIleAsnThrPheValArgTyrLeuLeuHisArgAla	140
DB	495	ATGTTCCAGAGCTTGGCGGAGCGCATCAACCTTGTGTAGGTACCTGCTGCACGCGGCC	554
QY	141	LysArgGlyLeuGlyMetArgHisAlaGluValSerMetAlaAsnMetValLeuIleGly	160
DB	555	AAGAAGGGCTGGCATGCGGCGCGCGAGCTGTCCATGGCCAACTGGTGTCTATCGGC	614
QY	161	PheValSerCysIleSerThrLeuCysIleGlyAlaAlaPheSerTyrTyrGluArg	180
DB	615	TTCTTCTCGTCATCAGCAGCTGTGCATCGGCGCGCGCTTCTCCCACTACGAGCAC	674
QY	181	TrpThrPhePheGlnAlaTyrTyrCysPheIleThrLeuThrThrIleGlyPheGly	200
DB	675	TGGACCTTCTTCAGGCTTACTACTGCTTCATCACCTCACCACCATCGGCTTCGGC	734
QY	201	AspTyrValAlaLeuGlnLysAspGlnAlaLeuGlnThrGlnProGlnTyrValAlaPhe	220
DB	735	GACTAGTGGCGCTGCAGAAGGACGAGGCGCTGCAGACGCGAGCTGCTGGCTTC	794
QY	221	SerPheValTyrIleLeuThrGlyLeuThrValIleGlyAlaPheLeuAsnLeuValVal	240
DB	795	AGCTTCGTCTACATCTTACGGGCTTCAGGTCATCGGCGCTTCTCAACCTCGTGGTG	854
QY	241	LeuArgPheMetThrMetAsnAlaGluAspGluLysArgAspAlaGluHisArgAlaLeu	260
DB	855	CTCGCTTTCATGACCATGAACCGCGAGGAGAGAGCGGACCGCGAGCACCGCGCGCTG	914
QY	261	LeuThrHisAsnGlyGlnAlaValGlyLeuGlyGlyLeuSerCysLeuSerGlySerLeu	280
DB	915	CTCAGCGCAACGGGCGGCGGCGGCGCGAGG-----GGT	953
QY	281	GlyAspValArgProArgAspProValThrCysAlaAlaAlaAlaGlyGlyValGlyVal	300
DB	954	GGCAGCGCGCACACTACGACACCGCGCTCATCCACGCGGCGAGCG-----998	
QY	301	GlyValGlyCysGlySerGlyPheArgAsnValTyrAlaGluValLeuHisPheGlnSerMet	320
DB	999	-----GGCGGCGGCGCTTCGCAACGCTTACGCGGAGGTGCTGCATTCAGTCCATG	1052
QY	321	CysSerCysLeuTrpTyrLysSerArgGluLysLeuGlnTyrSerIleProMetIleIle	340

; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 13502
 ; LENGTH: 88758
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-13502

Alignment Scores:
 Pred. No.: 1,19e-84 Length: 88758
 Score: 774.00 Matches: 169
 Percent Similarity: 61.80% Conservativity: 30
 Best Local Similarity: 52.48% Mismatches: 73
 Query Match: 36.77% Indels: 50
 DB: 4 Gaps: 5

US-09-939-483-5 (1-405) x US-09-949-016-13502 (1-88758)

Qy	92	GlyTyrGlyHisAlaProSerThrAspGlyGlyValPheCysMetPheTyrAla	111
Db	85915	GGTATGGGACGCTGCACCTGGCAGCATGGCGCAAGGCTTCTGCATGTTCTACGCC	85974
Qy	112	LeuLeuGlyLeuProLeuThrLeuLeuMetGlnSerLeuGlyGluArgLeuThr	131
Db	85975	GTGTCGGGCATCCGCTGCACACTGGTCATGTTCCAGAGCCCTGGCGAGGCATGAACACC	86034
Qy	132	PheValArgTyrLeuLeuHisArgAlaValArgGlyLeuGlyMetArgHisAlaGluVal	151
Db	86035	TTGTGGCTTACCTGCTGAAGCCGATTAAGAGTGCTGTGGCATGCGCAACTGACGTG	86094
Qy	152	SerMetAlaAsnMetValLeuLeuGlyPheValSerCysLeuSerThrLeuCysIleGly	171
Db	86095	TCTATGGAGAACATGGTGACTGTGGGCTTCTCTCTGCATGGGAGCGTGTGCATCGG	86154
Qy	172	AlaAlaAlaPheSerTyrTyrGluArgTyrPhePheGlnAlaTyrTyrCysPhe	191
Db	86155	GCGGCGCCCTTCTCCAGTGTGAGGAGTGGAGCTTCTTCCAGCCCTACTACTGCTTC	86214
Qy	192	IleThrLeuThrThrIleGlyPheGlyAspTyrValAlaLeuGlnLysAspGlnAlaLeu	211
Db	86215	ATCAGGTGTACTACCATTTGGGTTCGGGGACTAGTGGCCCTGCAGAACAGTGGGCTG	86274
Qy	212	GlnThrProGlnTyrValAlaPheSerPheValTyrIleLeuThrGlyLeuThrVal	231
Db	86275	CAGAGAGAGCGCTACTGCTGGGCTTTAGCTTTATGTATATCTGTGGGCTGACGGTC	86334
Qy	232	IleGlyAlaPheLeuLeuValValLeuArgPheMetThrMetAsnAlaGluAspGlu	251
Db	86335	ATCGGGCCCTTCTCAACCTGGTGGTCTCAGGTTCTTGACCAAGAAAGTGGAGTGA	86394
Qy	252	LysArgAspAlaGluHisArgAlaLeuLeuThrHisAsnGlyGlnAlaValGlyLeuGly	271
Db	86395	CGCGGGATGCTGAAGAGAGGGATCCCTCGCCGAAACCGCAAC	86439
Qy	272	GlyLeuSerCysLeuSerGlySerLeuGlyAspValArgProArgAspProValThrCys	291
Db	86440	-----AGCATGTGTCATTACATCCCTGAGGAGCCGGCGCCAGCCGCC-----	86484
Qy	292	AlaAlaAlaGlyGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyVal	311
Db	86485	-----AGGTACAAG	86493
Qy	312	AlaGluValLeuHisPheGlnSerMetCysSerCysLeuTyrTrpTyrLysSerArgGluLys	331
Db	86494	CGGACGTCCCGGACCTGCAGTCTGTGTGCTCTGCACCTGCTTACCGCTCGCAGGAC	86550

```
Db 310 GTGGCGGGAAGCTCTTCAACATGTGTATGCCATCGTGGGATTCCTCGGTCTCGTT 369
Qy 121 MetPheGlnSerLeuGlyGluArgIleAsnThrPheValArgTyrLeuLeuHisArgAla 140
Db 370 ATGTTCCAGACATCGGAGAAGAGTGAATAGACTGAGACGTATGTATCAAGCGCGTC 429
Qy 141 LysArgGlyLeuGlyMetArgHisAlaGluValSerMetAlaAsnMetValLeuIleGly 160
Db 430 CGCTCCTCGCTGCGCTGCAAGAGGACCGTGCCTCGGAGTGGACCTCATCTGNGT--- 486
Qy 161 PheValSerCysIleSerThrLeuCysIle-----GlyAlaAlaAlaPheSerTyrTyr 178
Db 487 ---GTGACCACACTCAGTTCGCTACGACTAGCTGGCGGTGCTGGCGCTTTTCCAAATTT 543
Qy 179 GluArgTrpThrPhePheGlnAlaTyrTyrCysPheIleThrLeuThrIleGly 198
Db 544 GAGGCTGGAGCTACTTCGATTAGTATATTACTGTTTATTACTTTTAACCACTATAGGC 603
Qy 199 PheGlyAspTyrValAlaLeuGlnLysAspGlnAlaLeuGlnThrGlnProGlnTyrVal 218
Db 604 TTTGGCAGCATGTTAGCCCTGCAGCGGACAATGCACCTGAACAGGAAGCCCGAATACGTG 663
Qy 219 AlaPheSerPheValTyrIleLeuThrGlyLeuThrValIleGlyAlaPheLeuAsnLeu 238
Db 664 ATGTTCCGCACTGATATTACTATTGTCCTGCCCATTTGGCGCGCTCGCTGAACCTG 723
Qy 239 ValValLeuArgPheMetThrMetAsnAlaGluAspGluLysArgAspAlaGluHisArg 258
Db 724 TTAGTACTTAGTTTGTACATGATACCGAGATGAGCGCCGAC----- 771
Qy 259 AlaLeuLeuThrHisAsnGlyGlnAlaValGlyLeuGlyLeuSerCysLeuSerGly 278
Db 772 -----GAGGCCAGGCCCATGCGCGCTGCAAGTGGCTGTGAAG 810
Qy 279 SerLeuGlyAspValArgProArgAspProValThrCysAlaAlaAlaGlyGlyVal 298
Db 811 CTGAGGCGCGATGTGATAACATCAACCGATTCCTGAGCGGCTACGAGGACACGAT 870
Qy 299 GlyValGlyValGlyGlySerGlyPheArgAsnValTyrAlaGluValLeuHisPheGln 318
Db 871 GGCCAACTCTGAACGAGC----- 900
Qy 319 SerMetCysSerCysLeu-----TrpTyrLysSerArgGluLysLeuGln 333
Db 901 TCCATGTGCTGCTGCCA-CTGCATCTGCTCAATGGCAACCGGCACAAAAAAGTAGCAA 959
Qy 334 TyrSerIleProMetIleIleProArgAspLeuSerThrSerAspThrCysValGluHis 353
Db 960 CTTGGAAAAGAACACGATGCAGAAAATCAATACAAGCTGAGGCAATCGCGACGCACAT 1019
Qy 354 SerHisSerSerProGlyGlyGly-----ArgTyrSer 365
Db 1020 ACGACACTTCTCGCGAGGTGGTGGCCATGCAGGATTTGNACTACGACTACGATACGCA 1079
Qy 366 AspThrProSerHisProCys 372
Db 1080 GAG---CTGCACACCCTTGC 1097
```

RESULT 7

```
US-09-949-016-60471/c
; Sequence 60471, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
```

```
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60471
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-60471

Alignment Scores:
Pred. No.: 2,18e-70 Length: 601
Score: 631.50 Matches: 131
Percent Similarity: 68.78% Conservative: 21
Best Local Similarity: 59.28% Mismatches: 42
Query Match: 30.00% Indels: 27
DB: 4 Gaps: 2
```

US-09-939-483-5 (1-405) x US-09-949-016-60471 (1-601)

```
Qy 110 TyrAlaLeuLeuGlyIleProLeuThrLeuIleMetPheGlnSerLeuGlyGluArgIle 129
Db 600 TAGCCCGTGTGGGCATCCCGCTGACACTGTGTATGTTCCAGAGCTTGGCGCAGCGCATG 541
Qy 130 AsnThrPheValArgTyrLeuLeuHisArgAlaLysArgGlyLeuGlyMetArgHisAla 149
Db 540 AACACCTTCGTGCGCTACCTGCTGAAGCGCATTTAAGAAGTGTCTGGCATGCGCAACACT 481
Qy 150 GluValSerMetAlaAsnMetValLeuIleGlyPheValSerCysIleSerThrLeuCys 169
Db 480 GAGCTGTCTATGGAGAACATGTTGACTGTGGGCTTCTCTCTGCACTGGGAGCGCTGTGC 421
Qy 170 IleGlyAlaAlaAlaPheSerTyrTyrGluArgTrpThrPhePheGlnAlaTyrTyrTyr 189
Db 420 ATCGGGCGCGCCCTCTCCAGTGTGAGAGTGGAGCTTCTTCACGCGCTACTACTAC 361
Qy 190 CysPheIleThrLeuThrIleGlyPheGlyAspTyrValAlaLeuGlnLysAspGln 209
Db 360 TGCTTCATCACGTTGACTACCATTTGGTTTCGGGGACTACGTGGCCCTGCAGACCAAGGY 301
Qy 210 AlaLeuGlnThrGlnProGlnTyrValAlaPheSerPheValTyrIleLeuThrGlyLeu 229
Db 300 GCCTCGCAGAAAGCGCTCTACGTGGCGCTTTAGCTTTATGTATATATCTCTGGTGGGCTG 241
Qy 230 ThrValIleGlyAlaPheLeuAsnLeuValValLeuArgPheMetThrMetAsnAlaGlu 249
Db 240 ACGTCTATCGGGCCCTCTCAACCTGCTGCTCCTCAGGTTCTTGACCATGAACAGTGAG 181
Qy 250 AspGluLysArgAspAlaGluHisArgAlaLeuLeuThrHisAsnGlyGlnAlaValGly 269
Db 180 GATGAGCGCGGATGCTGAAGAGAGGGCATCTCCCGCGAAACCGCAAC----- 130
Qy 270 LeuGlyLeuSerCysLeuSerGlySerLeuGlyAspValArgProArgAspProVal 289
Db 129 -----AGCATGTGTCATTACATCCCTCGAGGAGCGCGCGCCCGCGCC--- 85
Qy 290 ThrCysAlaAlaAlaGlyValGlyValGlyValGlyValGlySerGlyPheArgAsn 309
Db 84 -----AGG 82
Qy 310 ValTyrAlaGluValLeuHisPheGlnSerMetCysSerCysLeuTrpTyrLysSerArg 329
Db 81 TACAAGCGGACGCTCCCGGACCTGCAGTCTGTGTCTCTGCACTGTCTGCACTGCTGCGCAG 22
Qy 330 Glu 330
Db 21 GAC 19
```

RESULT 8

```
US-09-949-016-1497
; Sequence 1497, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
```

```
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1497
; LENGTH: 2710
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1497

Alignment Scores:
Pred. No.:      6,666-34      Length:      2710
Score:          354.50      Matches:    117
Percent Similarity: 44.61%      Conservative: 61
Best Local Similarity: 29.32%      Mismatches: 167
Query Match:      16.84%      Indels:     56
DB:                4          Gaps:        15

US-09-939-483-5 (1-405) x US-09-949-016-1497 (1-2710)

Qy      6 LeuAlaLeuValCysThrPheThrTyrLeuLeuValGlyAlaAlaValPheAspAla 25
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
669 GTTGCCATCTTTGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 728

Qy      26 LeuGluSerGluProGluMetIleGluArgGlnArgLeuGluLeuGluGlu--- 44
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
729 TTGGAGAGCCCTTTGGAGCAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 788

Qy      45 LeuArgAlaArgTyrAsnLeuSerGluGlyGlyTyrGluGluLeuGluArgValValLeu 64
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
789 CTGGGGATCATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 839

Qy      65 Arg---LeuLysProHisLeuAlaGlyVal----- 73
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
840 CATGCTCTTGTATGCTGACAAATCGGGAGTCAATAGGAAATCTTTTCAACAACAGC 899

Qy      74 ---GlnTTPArgPheAlaGlySerPheTyrPheAlaIleThrValIleThrThrIleGly 92
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
900 AGCCACTGGGACCTGGGAGTGTCTTTTCTTGTGGAATGTCTTACGACCATAGGG 959

Qy      93 TyrGlyHisAlaAlaProSerThrAspGlyGlyLysValPheCysMetPheTyrAlaLeu 112
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
960 TATGGGAATATTGCTCCGAGCAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1019

Qy      113 LeuGlyIleProLeuThrLeuIleMetPheGlnSerLeuGlyGluArgIleAsnThrPhe 132
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1020 TTGGGAATTCACCTCTTTGGTGTCTTATTGCTGGAATTTGGAGCACTTTGGAACCATC 1079

Qy      133 ValArgTyrLeuLeuHisArgAlaLys-----ArgGlyLeuGlyMetArgHisAla 149
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1080 TTTGGGAAGAGCATTCGAGAGTGTGGAAGAGTCTTTTCAAAAAAGCAAGTGTGAGTCA 1139

Qy      150 GluValSerMetAlaAsnMetValIleGlyPheValSerCysIleSerThrLeuCys 169
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1140 AAGATCCGGGTCACTCAACCATCTCTTGTGCGCGGTGCAATGTGTGTGTGTGTGAGC 1199

Qy      170 IleGlyAlaAlaAlaPheSerTyrTyrGluArgIleThrPhePheGlnAlaTyrTyr 189
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1200 ATCCCTGTCTCATCTTTAAGTACATCGAGGCGCTGGAGCGCTTGGAGTCCATTACTTT 1259

Qy      190 CysPheIleThrLeuThrIleGlyPheGlyAspTyrValAlaLeuGlnLysAspGln 209
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1260 GTGGTGGTCACTCTGACACCGTGGGCTTTGGTGTATTTTGTGGCA---GGGGGAACGCT 1316
```

```
Qy      210 AlaLeuGlnThrGlnProGlnInTyrValAlaPheSerPheValTyrIleLeuThrGlyLeu 229
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1317 GGCAATCAATTATCGGAGTGTGTATAAGCCCTAGTGTGTGTGTGTGTGTGTGTGTGTGT 1376

Qy      230 ThrValIleGlyAlaPheLeuAsnLeuVal-----ValLeuArgPheMetThrMetAsn 247
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1377 GCCTACTTTGAGCTGCTCCTCAGTATGATCGAGATTTGGCTTACGGGTTCCTGCAAAAAG 1436

Qy      248 AlaGluAspGluLysArgAspAlaGluHisArgAlaLeuLeuThrHisAsnGlyGlnAla 267
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1437 ACAAAAGAGAGGTGGGTGAA-----ATCAAGGCCCATGCGGCAGAGTG 1480

Qy      268 ValGlyLeuGlyGlyLeuSerCys-----LeuSerGlySerLeuGlyAspValArg 284
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1481 GAAGGC-----CAATGTCCAGGTGTGAGTTCGGGAGACACCGCGGAAGGCTCAG 1528

Qy      285 ProArgAspProValThrCysAlaAlaAlaAla-----GlyGlyValGly 299
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1529 CGTGGAGATCCAGATAGCTGACGCGGGCGGCCACCATCGCAGCATGGAGCGCCGCGC 1588

Qy      300 ValGlyValGlyGlySerGlyPheArgAsnValTyrAlaGluValLeuHisPheGlnSer 319
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1589 GCTGGGCTGGACGAGCGGCCCACTCACTGGACATGCTGTCCCGGAGAGCGCTCTGT 1648

Qy      320 MetCysSerCysLeuTyrTyrLysSerArgGluLysLeuGlnTyrSerIleProMetIle 339
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1649 CTTTGC---TGCCC-TGGACACCGCGCTTCAAGGCTCAT----- 1686

Qy      340 IleProArgAspLeuSerThrSer-----AspThrCysValGluHisSerHisSerSer 357
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1687 ---CCCAGGAGAGCATCAACACCGCGGCCAACCAACCTGCGCTGAAGGGCGCGGAGCAGC 1743

Qy      358 ProGlyGlyGlyGlyArgTyr-----SerAspThrProSerHisPro 371
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1744 TGAACAAGCATGGGCGAGGTGCGTCCGAGGACAAACATCATCAACAGTTCGGGTCCA 1800

RESULT 9
US-09-799-451-432
; Sequence 432, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yungqing
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/09/799,451
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 432
; LENGTH: 2730
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
```

```
; LOCATION: (473) .. (2086)
US-09-799-451-432

Alignment Scores:
Pred. No.: 6.75e-34 Length: 2730
Score: 354.50 Matches: 117
Percent Similarity: 44.61% Conservative: 61
Best Local Similarity: 29.32% Mismatches: 167
Query Match: 16.84% Indels: 56
DB: 4 Gaps: 15

US-09-939-483-5 (1-405) x US-09-799-451-432 (1-2730)

Qy 6 LeuAlaLeuValCysThrPheThrTyrLeuLeuValGlyAlaAlaValPheAspAla 25
Db 689 GTTGCCATCTTTGGTGTGGTGTCTACTTGTCTACTGGCGTCTGTCTTCGGGCA 748

Qy 26 LeuGluSerGluProGluMetIleGluArgGlnArgLeuGluArgGlnLeuGlu--- 44
Db 749 TTGGAGCAGCCCTTTGAGAGCAGCAGAGAAATACCATCGCTTGGAGAGCGGAATTC 808

Qy 45 LeuArgAlaArgTyrAsnLeuSerGluGlyGlyTyrGluGluLeuGluArgValValLeu 64
Db 809 CTGGGGATCATGCTGTGTGAGCC---CAGGAGCTGGAGCTTGATCCAG 859

Qy 65 Arg---LeuLysProHisLysAlaGlyVal----- 73
Db 860 CATGCTCTTGATGCTGACATGCGGGAGTCACTCAATAGGAACTCTTCAACAACAGC 919

Qy 74 ---GlnTrpArgPheAlaGlySerPheTyrPheAlaIleThrValIleThrIleGly 92
Db 920 AGCCACTGGGACCTCGGACGCGCTTTTCTTCTGCTGGAACGTGTCATTACGACCATAGG 979

Qy 93 TyrGlyHisAlaAlaProSerThrAspGlyGlyLysValPheCysMetPheTyrAlaLeu 112
Db 980 TATGGGAATATTGCTCGGACACTGAAGGAGGCAAAATCTTTGTATTTATATGCCATC 1039

Qy 113 LeuGlyIleProLeuThrLeuIleMetPheGlnSerLeuGlyGluArgIleAsnThrPhe 132
Db 1040 TTGGGAATTCACCTCTTTGGTCTTCTTATGCTGGAATTTGGACCAACTTGGNACCATC 1099

Qy 133 ValArgTyrLeuLeuHisArgAlaLys-----ArgGlyLeuGlyMetArgHisAla 149
Db 1100 TTTGGGAAAGCATTTGAAGAGTGGAGAGTCTTTTCGAAAAAGCAAGTGAGTCAGACC 1159

Qy 150 GluValSerMetAlaAsnMetValLeuIleGlyPheValSerCysIleSerThrLeuCys 169
Db 1160 AAGATCCGGGTCACTCAACCATCTGTTCATCTTGGCGCGCTGCTATTGTTGTGACG 1219

Qy 170 IleGlyAlaAlaAlaPheSerTyrTyrGluArgTrpThrPhePheGlnAlaTyrTyrTyr 189
Db 1220 ATCCCTGCTGCATCTTTAAGTACATCGAGGCTGGAGCGCTTGGAGTCCATTACTTT 1279

Qy 190 CysPheIleThrLeuThrIleGlyPheGlyAspTyrValAlaLeuGlnLysAspGln 209
Db 1280 GTGGTGTGTCATCTGACACCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1336

Qy 210 AlaLeuGlnThrGlnProGlnTyrValAlaPheSerPheValTyrIleLeuThrGlyLeu 229
Db 1337 GGCATCAATATATCGGGAGTGTATTAAGCCCTAGTGGTGGTGGTGGTGGTGGTGGTGG 1396

Qy 230 ThrValIleGlyAlaPheLeuAsnLeuVal-----ValLeuArgPheMetThrMetAsn 247
Db 1397 GCCTACTTTGACGTGCTCCTCAGTATGATCGGAGATGGCTACGGTTCGTCCAAAAG 1456

Qy 248 AlaGluAspGluLysArgAspAlaGluHisArgAlaLeuThrHisAsnGlyGlnAla 267
Db 1457 ACAAAAGAAGAGGTGGGTGAA-----ATCAAGGCCCATGCGGAGAGTGC 1500

Qy 268 ValGlyLeuGlyLeuSerCys-----LeuSerGlySerLeuGlyAspValArg 284
Db 1501 GAAGGC-----CAATGTACAGGCTGAGTTCGGGAGACACAGCGGCAAGGCTCAG 1548
```

```
285 ProArgAspProValThrCysAlaAlaAlaAla-----GlyGlyValGly 299
1549 CGTGGAGATCCAGATAAGCTGAGCGGGGGCCACCATCCGCGAGCATGGAGCGCGCG 1608

300 ValGlyValGlyGlySerGlyPheArgAsnValTyrAlaGluValLeuHisPheGlnSer 319
1609 GCTGGGCTCGGACGAGCGGCGCCACTCACTGGGACATGCTGTCTCCCGAGAGGCTCTGT 1668

320 MetCysSerCysLeuTrpTyrLysSerArgGluLysLeuGlnTyrSerIleProMetIle 339
1669 CTTTGC---TGCCC-TGGACACCGGCGCTTCAAGGCCTCAT----- 1706

340 IleProArgAspLeuSerThrSer-----AspThrCysValGluHisSerHisSerSer 357
1707 ---CCCAGAGAGCATCAACACCGGCCCAACAACCTGCGCCTGAAGGGSCCGAGCAGC 1763

358 ProGlyGlyGlyGlyArgTyr-----SerAspThrProSerHisPro 371
1764 TGAACAAGCATGGCGAGGTGCGTCCGAGGACAAACATCATCAACAAGTTGCGGTCCA 1820

RESULT 10
US-09-949-016-1130
; Sequence 1130, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1130
; LENGTH: 2730
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1130

Alignment Scores:
Pred. No.: 6.75e-34 Length: 2730
Score: 354.50 Matches: 117
Percent Similarity: 44.61% Conservative: 61
Best Local Similarity: 29.32% Mismatches: 167
Query Match: 16.84% Indels: 56
DB: 4 Gaps: 15

US-09-939-483-5 (1-405) x US-09-949-016-1130 (1-2730)

Qy 6 LeuAlaLeuValCysThrPheThrTyrLeuLeuValGlyAlaAlaValPheAspAla 25
Db 689 GTTGCCATCTTTGGTGTGGTGTCTACTTGTCTACTGGCGTCTGTCTTCGGGCA 748

Qy 26 LeuGluSerGluProGluMetIleGluArgGlnArgLeuGluGlnLeuGlu--- 44
Db 749 TTGGAGCAGCCCTTTGAGAGCAGCAGAGAAATACCATCGCTTGGAGAGCGGAATTC 808

Qy 45 LeuArgAlaArgTyrAsnLeuSerGluGlyGlyTyrGluGluLeuGluArgValValLeu 64
Db 809 CTGGGGATCATGCTGTGTGAGCC---CAGGAGCTGGAGCTTGATCCAG 859

Qy 65 Arg---LeuLysProHisLysAlaGlyVal----- 73
Db 860 CATGCTCTTGATGCTGACATGCGGGAGTCACTCAATAGGAACTCTTCAACAACAGC 919

Qy 74 ---GlnTrpArgPheAlaGlySerPheTyrPheAlaIleThrValIleThrIleGly 92
Db 920 AGCCACTGGGACCTCGGACGCGCTTTTCTTCTGCTGGAACGTGTCATTACGACCATAGG 979

Qy 93 TyrGlyHisAlaAlaProSerThrAspGlyGlyLysValPheCysMetPheTyrAlaLeu 112
Db 980 TATGGGAATATTGCTCGGACACTGAAGGAGGCAAAATCTTTGTATTTATATGCCATC 1039

Qy 113 LeuGlyIleProLeuThrLeuIleMetPheGlnSerLeuGlyGluArgIleAsnThrPhe 132
Db 1040 TTGGGAATTCACCTCTTTGGTCTTCTTATGCTGGAATTTGGACCAACTTGGNACCATC 1099

Qy 133 ValArgTyrLeuLeuHisArgAlaLys-----ArgGlyLeuGlyMetArgHisAla 149
Db 1100 TTTGGGAAAGCATTTGAAGAGTGGAGAGTCTTTTCGAAAAAGCAAGTGAGTCAGACC 1159

Qy 150 GluValSerMetAlaAsnMetValLeuIleGlyPheValSerCysIleSerThrLeuCys 169
Db 1160 AAGATCCGGGTCACTCAACCATCTGTTCATCTTGGCGCGCTGCTATTGTTGTGACG 1219

Qy 170 IleGlyAlaAlaAlaPheSerTyrTyrGluArgTrpThrPhePheGlnAlaTyrTyrTyr 189
Db 1220 ATCCCTGCTGCATCTTTAAGTACATCGAGGCTGGAGCGCTTGGAGTCCATTACTTT 1279

Qy 190 CysPheIleThrLeuThrIleGlyPheGlyAspTyrValAlaLeuGlnLysAspGln 209
Db 1280 GTGGTGTGTCATCTGACACCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1336

Qy 210 AlaLeuGlnThrGlnProGlnTyrValAlaPheSerPheValTyrIleLeuThrGlyLeu 229
Db 1337 GGCATCAATATATCGGGAGTGTATTAAGCCCTAGTGGTGGTGGTGGTGGTGGTGGTGG 1396

Qy 230 ThrValIleGlyAlaPheLeuAsnLeuVal-----ValLeuArgPheMetThrMetAsn 247
Db 1397 GCCTACTTTGACGTGCTCCTCAGTATGATCGGAGATGGCTACGGTTCGTCCAAAAG 1456

Qy 248 AlaGluAspGluLysArgAspAlaGluHisArgAlaLeuThrHisAsnGlyGlnAla 267
Db 1457 ACAAAAGAAGAGGTGGGTGAA-----ATCAAGGCCCATGCGGAGAGTGC 1500

Qy 268 ValGlyLeuGlyLeuSerCys-----LeuSerGlySerLeuGlyAspValArg 284
Db 1501 GAAGGC-----CAATGTACAGGCTGAGTTCGGGAGACACAGCGGCAAGGCTCAG 1548
```

Db 920 ACCCACTGGACCTCGGAGTCCTTTTCTTGTGGAAGTGTCAATACGACCATAGG 979
Qy 93 TyrGlyHisAlaAlaProSerThrAspGlyValPheCysMetPheThrAlaLeu 112
Db 980 TATGGAAATATGCTCCGAGCACTAAGGAGCAAAATCTTTGATTTATATGCCATC 1039
Qy 113 LeuGlyIleProLeuThrLeuIleMetPheGlnSerLeuGlyGluArgIleAsnThrPhe 132
Db 1040 TTGGAAATCCACTCTTTGGTTCTTATTGCTGAATTTGGAGACCACTTGGAAACCATC 1099
Qy 133 ValArgTyrLeuLeuHisArgAlaLys-----ArgGlyLeuGlyMetArgHisAla 149
Db 1100 TTGGGAAAGCATTTGCAAGAGTGGAGAGGTCTTTGAAAAGCAAGTGAAGTCAAGACC 1159
Qy 150 GluValSerMetAlaAsnMetValLeuIleGlyPheValSerCysIleSerThrLeuCys 169
Db 1160 AAGATCCGGTCACTCAACCATCTGTTTCATCTTGGCCGGTGCATTTGTTGTGACG 1219
Qy 170 IleGlyAlaAlaAlaPheSerTyrTyrGluArgTyrPhePheGlnAlaTyrTyr 189
Db 1220 ATCCCTGCTGCATCTTTAAGTACATCGAGGCTGGAGCGCTTGGAGTCCATTTACTTT 1279
Qy 190 CysPheIleThrLeuThrThrIleGlyPheGlyAspTyrValAlaLeuGlnLysAspGln 209
Db 1280 GTGGTGGTCACTCTGACCAACCGTGGCTTTGGTGAATTTGTGGCA---GGGGGAAACGCT 1336
Qy 210 AlaLeuGlnThrGlnProGlnTyrValAlaPheSerPheValTyrIleLeuThrGlyLeu 229
Db 1337 GGCATCAATATTCGGGAGTGGTATTAAGCCCTAGTGTGTTTGGATCTTTGTTGGCCTT 1396
Qy 230 ThrValIleGlyAlaPheLeuAsnLeuVal-----ValLeuArgPheMetThrMetAsn 247
Db 1397 GCCTACTTTGACGCTGCTCAGTATGATCGAGATTGGCTACGGGTTCTCTCCAAAAAG 1456
Qy 248 AlaGluAspGluLysArgAspAlaGluHisArgAlaLeuThrHisAsnGlyGlnAla 267
Db 1457 ACAAAAGAGAGTGGGTGAA-----ATCAAGGCCCATGCGGAGAGTGTG 1500
Qy 268 ValGlyLeuGlyGlyLeuSerCys-----LeuSerGlySerLeuGlyAspValArg 284
Db 1501 GAAGGC-----CAATGTCAAGCTGAGTTCGGGAGACACGCGGAGGCTCAG 1548
Qy 285 ProArgAspProValThrCysAlaAlaAla-----GlyGlyValGly 299
Db 1549 CGTGAGATCCACGATAGCTGCAGCGCGCGGCCACCATCCGAGCATGGAGCGCGGCG 1608
Qy 300 ValGlyValGlyGlySerGlyPheArgAsnValTyrAlaGluValLeuHisPheGlnSer 319
Db 1609 GCTGGCTCGACCGCGCGGCCACTCTAGACATGCTGTCCCGGAGAGCGCTCTGT 1668
Qy 320 MetCysSerCysLeuTyrTyrLysSerArgGluLysLeuGlnTyrSerIleProMetile 339
Db 1669 CTTTGC---TGCCC-TGGACACCGCGCGCTTCAAGGCCTCAT----- 1706
Qy 340 IleProArgAspLeuSerThrSer-----AspThrCysValGluHisSerHisSerSer 357
Db 1707 ---CCCAGGAGCATCAACAACCGGCCCAACACCTCGCGCTGAAGGGCGCGGAGCAGC 1763
Qy 358 ProGlyGlyGlyValArgTyr-----SerAspThrProSerHisPro 371
Db 1764 TGACACAGCATGGGAGGCTGGTCCGAGGACAAACATCATCAAGTTCCGGGTCCA 1820

RESULT 11
US-09-362-842-13
; Sequence 13, Application US/09362842
; Patent No. 6511824
; GENERAL INFORMATION:
; APPLICANT: Buchman et al.
; TITLE OF INVENTION: NUCLEIC ACIDS AND POLYPEPTIDES OF INVERTEBRATE TWIK
; TITLE OF INVENTION: CHANNELS AND METHODS OF USE
; FILE REFERENCE: 7326-104
; CURRENT APPLICATION NUMBER: US/09362,842
; CURRENT FILING DATE: 1999-07-28

; PRIOR APPLICATION NUMBER: 09/270,767
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1086
; TYPE: DNA
; ORGANISM: Leptinotarsa decemlineata
US-09-362-842-13

Alignment Scores:
Pred. No.: 1,49e-34 Length: 1086
Score: 354.00 Matches: 102
Percent Similarity: 46.69% Conservative: 53
Best Local Similarity: 30.72% Mismatches: 111
Query Match: 16.82% Indels: 66
DB: 4 Gaps: 11

US-09-939-483-5 (1-405) x US-09-362-842-13 (1-1086)

Qy 13 PheThrTyrLeuLeuValGlyAlaAlaValPheAspAlaLeuGluSerGluProGluMet 32
Db 160 TTCAATGTTTGTGTAGCGGAGCAGCGTTTTCAGTTTACTTTTGAGGCACCTTGAGCAACGG 219
Qy 33 IleGluArgGlnArgLeuGluLeuArg---GlnLeuGluLeuArgAlaArgTyrAsnLeu 51
Db 220 GCACTGAGAGTTAACTTTGGAACGAGTAGTACAAAAATTTTGGTGTCTTAATCTCTAAGCTT 279
Qy 52 SerGluGlyTyrGluGluGluValValLeuArgValValLeuArgLeuLysProHisLysAla 71
Db 280 ACAGATCCAGATTGGGAAGAATTG-----ATAGTAAATAGTGAGAGCAAAATAATCGT 333
Qy 72 GlyVal-----GlnTyrArgPheAlaGlySerPhe 81
Db 334 GGAGTTTCAGCTATCGAAAATGCCACTTCAGAGCCTAATTTGGAGCTTTTGGTCAATCATTT 393
Qy 82 TyrPheAlaIleThrValIleThrIleGlyTyrGlyHisAlaAlaProSerThrAsp 101
Db 394 TTCTTTCCAGCAGCAGTCATCACAACTATAGGATATGTCATGTACTCCACTCAGCAGA 453
Qy 102 GlyGlyLysValPheCysMetPheTyrAlaLeuGlyIleProLeuThrLeuIleMet 121
Db 454 AATGGTAAATATTTTCATGTTTATGCGGTGTGGAAATTCCTTTGACTCTCGTACTG 513
Qy 122 PheGlnSerLeuGlyGluArgIleAsnThrPheValArgTyrLeuLeuHis-----Arg 139
Db 514 CTTTCTGCTCTCGGGAACGATTACTGATTCGAGAGTTTGGCTCTTGCATGCTTAAT 573
Qy 140 AlaLysArgGlyLeuGlyMetArgHisAlaGluValSerMetAlaAsnMetValLeuIle 159
Db 574 TCAAAATTAGGACACCTTTATCAGCCTCTTCGAATACGAATCGTCCATTTGGCAATTATA 633
Qy 160 GlyPheValSerCysIleSerThrLeuCysIleGlyAlaAlaAlaPheSerTyrTyrGlu 179
Db 634 GTTTTAGTACTATTGATTCTCTCTGCTACTCCAGCTGCATTTTGGCTTTGGCTTTGGAA 693
Qy 180 ---ArgTyrThrPhePheGlnAlaTyrTyrCysPheIleThrLeuThrIleGly 198
Db 694 CCAGAAATGGGACTATTGTTGATTCTCTTACTATTGCTTTATATCCCTCACAACAATAGGA 753
Qy 199 PheGlyAspTyrValAlaLeuGlnLysAspGlnAlaLeuGlnThr---GlnProGlnTyr 217
Db 754 TTGGGAGACTACATTT-----CCTGGAGATTCCGCCCCAGCCCTTACCGCTTTTATAC 807
Qy 218 ValAlaPheSerPheValTyrIleLeuThrThrValIleGlyAlaPheLeuAsn 237
Db 808 AAAATAATGACTACATGTTTACCTTTCTCGGGTATAACAATAATG-----ATGTTGACG 861
Qy 238 LeuValVal-----LeuArgPheMetThrMetAsnAlaGlu 249
Db 862 CTAACAGATTTTACGATATACCCCACTCAATTTGGCGCTACTCTTCACAACTAGCGAA 921
Qy 250 AspGluLysArgAspAlaGluHisArgAlaLeuLeuThrHisAsnGlyGlnAlaValGly 269

```

Db      922 GACTCTGAAGAAA----- 933
Qy      270 LeuGlyLeuSerCysLeuSerGlySerLeuGlyAspValArgProArgAspProVal 289
Db      934 -----GTG 936
Qy      290 ThrCysAlaAlaAlaGlyGlyValGlyValGlyValGlyGlySerGlyPheArg--- 308
Db      937 AGTTAGCCAGTTCCGGCCNGGTTTACGTACGGACGAGGTTTTCGCCCTCATATGAA 996
Qy      309 ---AsnValTyrAlaGluValLeuHisPheGlnSer 319
Db      997 GATAATATCCACCACCAAGTAGTGAGGTTAGATCG 1032

RESULT 12
US-09-236-080-5
; Sequence 5, Application US/09236080
; Patent No. 6242217
; GENERAL INFORMATION:
; APPLICANT: Helen Meadows
; APPLICANT: Conrad Chapman
; TITLE OF INVENTION: NO. 6242217el Compounds
; FILE REFERENCE: GP30031
; CURRENT APPLICATION NUMBER: US/09/236.080
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1994
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-236-080-5

Alignment Scores:
Pred. No.: 6.23e-33 Length: 1994
Score: 345.00 Matches: 90
Percent Similarity: 51.54% Conservative: 96
Best Local Similarity: 30.72% Mismatches: 96
Query Match: 16.39% Indels: 46
DB: 3 Gaps: 10

US-09-939-483-5 (1-405) x US-09-236-080-5 (1-1994)
Qy      1 GluAsnValArgThrLeuAlaLeuValCysThrPheThrTyrLeuLeuValGlyAla 20
Db      616 AAGACAGTCTCCACGATTTCTCGTGTGTC-----GTCTCTACCTGATCATCGGAGCC 669
Qy      21 AlaValPheAspAlaLeuGluSerGluProGluMetIleGluArgGlnArgLeuGluLeu 40
Db      670 GCGGTGTTCAAGGCAATTGGAGCAGCTTCAGAGATTTCCAGAGAGACCACCATTTGTATC 729
Qy      41 ArgGlnLeuGluLeuArgAlaArgTyr-----AsnLeuSerGluGlyGlyTyrGlu 57
Db      730 CAGAAGCAGACCTTTCATAGCCACGATGCTGCGTCAACTCCACCGAGCTGGAC---GAA 786
Qy      58 GluLeuGluArgValLeuArgLeuLysProHisAlaGlyVal----- 73
Db      787 CTCAATCAGCAAAATAGTGGCAGCAATA-----AACGAGGAGATATCCCTTAGGA 837
Qy      74 -----GlnTrpArgPheAlaGlySerPheTyrPheAlaIleThr 86
Db      838 AACAGCTCCATCAAGTTAGTCACTGGGACCTCGGAGCTCTTCTCTTTGCTGTACT 897
Qy      87 ValIleThrThrIleGlyTyrGlyHisAlaAlaProSerThrAspGlyGlyLysValPhe 106
Db      898 GTTATCAACACATAGAGTTTGGAAACATCTCCCCACGAACTGAAGGTGGAAAAATATTC 957
Qy      107 CysMetPheTyrAlaLeuLeuGlyIleProLeuThrLeuIleMetPheGlnSerLeuGly 126
Db      958 TGCATCATCTATGCTTGTGGAAATTCCTCTTTGCTGCTTTCTGCTGCTGCTGCTGCTGCT 1017
Qy      127 GluArgIle-----AsnThrPheValArg 134
; Sequence 1, Application US/09432470
; Patent No. 6426197
; GENERAL INFORMATION:
; APPLICANT: David Malcolm Duckworth
; APPLICANT: Conrad Gerald Chapman
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30190
; CURRENT APPLICATION NUMBER: US/09/432,470
; CURRENT FILING DATE: 1999-11-03
; EARLIER FILING DATE: 1999-10-07
; EARLIER APPLICATION NUMBER: UK 9824048.4
; EARLIER FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1182
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-432-470-1

Alignment Scores:
Pred. No.: 7.87e-33 Length: 1182
Score: 341.00 Matches: 105
Percent Similarity: 44.54% Conservative: 50
Best Local Similarity: 30.17% Mismatches: 127
Query Match: 16.20% Indels: 67
DB: 3 Gaps: 10

US-09-939-483-5 (1-405) x US-09-432-470-1 (1-1182)
Qy      6 LeuAlaLeuIleValCysThrPheThrTyrLeuLeuValGlyAlaAlaValPheAspAla 25
Db      19 CTGGCCCTGCTGGCGCTGTGCTTTGCTTTTACTGTGTCTGTGCTGCTGCTGCTGCTGCTG 78
Qy      26 LeuGluSerGluProGlu---MetIleGluArgGlnArgLeuGluLeuArgGlnLeuGlu 44
Db      79 CTGAGCAGCCCCACGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 138
Qy      45 LeuArgAlaArgTyrAsnLeuSerGlu----- 53
; Sequence 1, Application US/09432470
; Patent No. 6426197
; GENERAL INFORMATION:
; APPLICANT: David Malcolm Duckworth
; APPLICANT: Conrad Gerald Chapman
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30190
; CURRENT APPLICATION NUMBER: US/09/432,470
; CURRENT FILING DATE: 1999-11-03
; EARLIER FILING DATE: 1999-10-07
; EARLIER APPLICATION NUMBER: UK 9824048.4
; EARLIER FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1182
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-432-470-1

Alignment Scores:
Pred. No.: 7.87e-33 Length: 1182
Score: 341.00 Matches: 105
Percent Similarity: 44.54% Conservative: 50
Best Local Similarity: 30.17% Mismatches: 127
Query Match: 16.20% Indels: 67
DB: 3 Gaps: 10

US-09-939-483-5 (1-405) x US-09-432-470-1 (1-1182)
Qy      6 LeuAlaLeuIleValCysThrPheThrTyrLeuLeuValGlyAlaAlaValPheAspAla 25
Db      19 CTGGCCCTGCTGGCGCTGTGCTTTGCTTTTACTGTGTCTGTGCTGCTGCTGCTGCTGCTG 78
Qy      26 LeuGluSerGluProGlu---MetIleGluArgGlnArgLeuGluLeuArgGlnLeuGlu 44
Db      79 CTGAGCAGCCCCACGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 138
Qy      45 LeuArgAlaArgTyrAsnLeuSerGlu----- 53
```



```
Db 139 CTGAGGGCCATCCCTGTGTGAGCAGCAGGAGCTGGGCTCTCTCATCAAGAGGTGGCT 198
Qy 54 -----GlyGlyTyrGluGluLeuGluArgValValLeuArgLeuLysProHisLys 70
Db 199 GATGCCCTGGAGGGGTGGGAGCCAGAAACCAACTCGACCAAGCAAGCAGCAGCCACTCA 258
Qy 71 AlaGlyValGlnTyrArgPheAlaGlySerPheTyrPheAlaIleThrValIleThrThr 90
Db 259 GCC-----TGGAGCTGGGAGCGGCTCTCTTTCTCAGGAGCCATCACCACC 309
Qy 91 IleGlyTyrGlyHisAlaAlaProSerThrAspGlyGlyLysValPheCysMetPheTyr 110
Db 310 ATCGGCTATGCAATGTGGCTCGGCACAGATGCGGGCGGCTCTCTGATCTTTAT 369
Qy 111 AlaLeuLeuGlyIleProLeuThrLeuIleMetPheGlnSerLeuGlyGluArgIleAsn 130
Db 370 CGCGTGTGGGATTCGCTGTTGGGATCTTACTTGGCAGGGGTGGGGACCGCTGGGC 429
Qy 131 ThrPheValArgTyrLeuLeuHisArgAlaLysArgGlyLeuGlyMetArgHisAlaGlu 150
Db 430 TCCTCCCTGGCCCAT-----GGCATCGGTCAATTGAA 462
Qy 151 -----ValSerMetAlaAsnMetValLeu 158
Db 463 GCCATCTTCTGAAGTGCACGTGCCACCGGAGTAGTAAGAGTGTCTGGCGATGCTT 522
Qy 159 IleGlyPheValSerCysIleSerThrLeuCysIleGlyAlaAlaAlaPheSerTyr 178
Db 523 TTCTGCTGTATCGGCTGCTCTTGTCTCTCAGCCACAGTTCGTGTTCTGTATATG 582
Qy 179 GluArgTrpThrPhePheGlnAlaTyrTyrCysPheIleThrLeuThrThrIleGly 198
Db 583 GAGGACTGGAGCAAGCTGGAGGCCATCTACTTTGTTCATAGTGACGCTTACCACCGTGGC 642
Qy 199 PheGlyAspTyrValAlaLeuGlnLysAspGlnAlaLeuGlnThrGlnProGlnTyrVal 218
Db 643 TTGGCGACTATGGCCGGCGGAGCCAG-----CAGGACTCCCGGCGCTATCAG 696
Qy 219 AlaPheSerPheValTyrIleLeuThrGly-----LeuThrVal 231
Db 697 CGCGTGGTGTGTTCTGGATCTCTGCTGGCTGGCTTACTTTCGCTCAGTGTCTCACCAC 756
Qy 232 IleGlyAlaPheLeuAsnLeuValValLeuArgPheMetThrMetAsnAla----- 248
Db 757 ATCGGAACTGGCTGCGAGTAGTGTCCCGCGCACTCGGGCAGA-GATGGGCGGCGCTCAC 815
Qy 249 -----GluAspGluLysArgAspAlaGluHisArgAla 259
Db 816 GGCTCAGGCTGCCAGCTGGACAGTGGACAGCGCGGTGACCCAGCGAGCGGGGCC 875
Qy 260 LeuLeuThrHisAsnGlyGlnAlaValGlyLeuGlyLeuSerCysLeuSerGlySer 279
Db 876 CGCCGCCCGCGCGGAGAGGAGGAGCACCCTGCTGCTCCACCGGCTGTCCAGCGCA 935
Qy 280 LeuGly-----AspValArgProArgAspProValThrCysAlaAlaAla 294
Db 936 CGCGTGGGAGGCGCCGATCCCTTTCGCCCGCGGAGAGGC---TCAGCGCGCTTCCCC 992
Qy 295 AlaGlyGlyValGlyValGlyVal 302
Db 993 GCCACGCGCTCGGCGCTGGATTA 1016
```

RESULT 14

```
US-09-432-470-3
; Sequence 3, Application US/09432470
; Patent No. 6426197
; GENERAL INFORMATION:
; APPLICANT: David Malcolm Duckworth
; APPLICANT: Conrad Gerald Chapman
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30190
; CURRENT APPLICATION NUMBER: US/09/432,470
```

```
; CURRENT FILING DATE: 1999-11-03
; EARLIER APPLICATION NUMBER: UK 9923668.9
; EARLIER FILING DATE: 1999-10-07
; EARLIER APPLICATION NUMBER: UK 9824048.4
; EARLIER FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1218
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-432-470-3

Alignment Scores:
Pred. NO.: 8.31e-33 Length: 1218
Score: 341.00 Matches: 105
Percent Similarity: 44.54% Conservative: 50
Best Local Similarity: 30.17% Mismatches: 127
Query Match: 16.20% Indels: 67
DB: 3 Gaps: 10

US-09-939-483-5 (1-405) x US-09-432-470-3 (1-1218)

Qy 6 LeuAlaLeuIleValCysThrPheThrLeuLeuValGlyAlaAlaValPheAspAla 25
Db 55 CTGCCCCCTGCTGGCGCTGTGCTTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 114
Qy 26 LeuGluSerGluProGlu---MetIleGluArgGlnArgLeuGluLeuArgGlnLeuGlu 44
Db 115 CTGGAGCAGCCCCCAGCAGCAGCAGGCGCCAGAGGAGCTGGGGAGGTCGAGAGAAGTTC 174
Qy 45 LeuArgAlaArgTyrAsnLeuSerGlu----- 53
Db 175 CTGAGGGCCCATCCGCTGTGTGAGCGCAGCAGGAGCTGGGCTCTCTCATCAAGAGGTGGCT 234
Qy 54 -----GlyGlyTyrGluGluLeuGluArgValValLeuArgLeuLysProHisLys 70
Db 235 GATGCCCTGGAGGGGTGGGAGCCAGAAACCACTCGACCAAGCAGCAGCAGCAGCTCA 294
Qy 71 AlaGlyValGlnTyrArgPheAlaGlySerPheTyrPheAlaIleThrValIleThrThr 90
Db 295 GCC-----TGGACCTGGGCGGCGCTCTCTTTCTCAGGAGCCATCATCACCACC 345
Qy 91 IleGlyTyrGlyHisAlaAlaProSerThrAspGlyGlyLysValPheCysMetPheTyr 110
Db 346 ATCGGCTATGCAATGTGGCGCTCGCAGCAGATCGCGGCGGCTCTTCTGTCATCTTTAT 405
Qy 111 AlaLeuLeuGlyIleProLeuThrLeuIleMetPheGlnSerLeuGlyGluArgIleAsn 130
Db 406 CGCGTGTGGGATTCGCTGTTTGGGATCTTCTGCGAGGGGTGGGGAGCCGCTGGGC 465
Qy 131 ThrPheValArgTyrLeuLeuHisArgAlaLysArgGlyLeuGlyMetArgHisAlaGlu 150
Db 466 TCCTCCCTGGCCCAT-----GGCATCGGTCAATTGAA 498
Qy 151 -----ValSerMetAlaAsnMetValLeu 158
Db 499 GCCATCTTCTGAAGTGGCAGCTGCCAGCGAGTAGTAAGAGTGTCTGCGCATGCTT 558
Qy 159 IleGlyPheValSerCysIleSerThrLeuCysIleGlyAlaAlaAlaPheSerTyr 178
Db 559 TTCTGCTGATCGGCTGCTGCTTGTCTCAGCGCCAGGTCGTGCTGCTGCTATATG 618
Qy 179 GluArgTrpThrPhePheGlnAlaTyrTyrCysPheIleThrLeuThrThrIleGly 198
Db 619 GAGGACTGGAGCAAGCTGGAGGCCATCTACTTTGTTCATAGTACGCTTACCACCGTGGC 678
Qy 199 PheGlyAspTyrValAlaLeuGlnLysAspGlnAlaLeuGlnThrGlnProGlnTyrVal 218
Db 679 TTTGGCGACTATGTGGCGGCGGAGCCAGG-----CAGGACTCCCGGCGCTATCAG 732
Qy 219 AlaPheSerPheValTyrIleLeuThrGly-----LeuThrVal 231
Db 219 AlaPheSerPheValTyrIleLeuThrGly-----LeuThrVal 231
```

```
Db 733 CCGCTGTGTGGTCTTGATCCTGCTGGCGCTGCTTACTTGGCTCAGTCTCAGCCACC 792
Qy 232 ILeGlyAlaPheLeuAsnLeuValValLeuArgPheMetThrMetAsnAla----- 248
Db 793 ATCGGGAAGTGGTGGCAGTAGTGTCCGCGCACTCGGCGAGA-GATGGGCGGCTTCAC 851
Qy 249 -----GluAspGluLysArgAspAlaGluHisArgAla 259
Db 852 GGCTCAGGCTGCCAGCTGGACTGGCAGCAGTGCAGCGCGGTGACCCAGCAGCGGGGCC 911
Qy 260 LeuLeuThrHisAenGlyGlnAlaValGlyLeuGlyLeuSerCysLeuSerGlySer 279
Db 912 CGCGCGCGCGCGCGAGAGGAGCAGCAGCAGTCTGCTCCACCGCCCTGTCCAGCGCA 971
Qy 280 LeuGly-----AspValArgProArgAspProValThrCysAlaAlaAla 294
Db 972 GCGCTGGGCGAGCGCCGATCCCTTCGCCCCCGAGAGAGC---TCAGCGGCTTCCCC 1028
Qy 295 AlaGlyGlyValGlyValGlyVal 302
Db 1029 GCCCAGCGCTCGGCCCTGGATTA 1052

RESULT 15
US-09-949-016-1938
; Sequence 1938, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1938
; LENGTH: 2733
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1938

Alignment Scores:
Pred. No.: 3,55e-32 Length: 2733
Score: 341.00 Matches: 105
Percent Similarity: 44.54% Conservative: 50
Best Local Similarity: 30.17% Mismatches: 127
Query Match: 16.20% Indels: 67
DB: 4 Gaps: 10

US-09-939-483-5 (1-405) x US-09-949-016-1938 (1-2733)
Qy 6 LeuAlaLeuValCysThrPheThrLeuLeuValGlyAlaAlaValPheAspAla 25
Db 160 CTGGCCCTGTGGCGCTGGTCTTCTTACTTGTGTCTGTGGTGGCTTCCGGGCC 219
Qy 26 LeuGluSerGluProGlu---MetIleGluArgGlnArgLeuGluLeuArgGlnLeuGlu 44
Db 220 CTGGAGCAGCCCCAGCAGCAGCAGCGGCTGGGGAGGTCCGAGAGAGTTC 279
Qy 45 LeuArgAlaArgTyrAsnLeuSerGlu----- 53
Db 280 CTGAGGGCCCATCGTGTGTGAGCGACCCAGGAGCTGGGGAGGTCCGAGAGAGTTC 339
Qy 54 -----GlyGlyTyrGluGluLeuGluArgValValLeuArgLeuLysProHisLys 70
Db 340 GATGCCCTGGAGGGGGTGGCGGACCCAGAAACCAACTCGACCCAGCAACAGCAGCACTCA 399
```

```
Qy 71 AlaGlyValGlnTrpArgPheAlaGlySerPheThrPheAlaIleThrValIleThr 90
Db 400 GCC-----TGGACCTGGGCACGCGCTCTTTTCTCAGGAGCATCATCACCACC 450
Qy 91 IleGlyTyrGlyHisAlaAlaProSerThrAspGlyGlyLysValPheCysMetPheTyr 110
Db 451 ATCGGCTATGGCAATGGCCCTGCGCAGACAGATGCGGGCGCCTCTTCGTCATCTTTAT 510
Qy 111 AlaLeuLeuGlyIleProLeuThrLeuIleMetPheGlnSerLeuGlyGluArgIleAsn 130
Db 511 GCGCTGGTGGGATTCGCTGTTGGATCTCTACTCGCAGGGGTGCGGACCGGCTGGGC 570
Qy 131 ThrPheValArgTyrLeuLeuHisArgAlaLysArgGlyLeuGlyMetArgHisAlaGlu 150
Db 571 TCCTCCTCGGCCCAT-----GGCATCGGTCACTTGAA 603
Qy 151 -----ValSerMetAlaAsnMetValLeu 158
Db 604 GCCATCTTCTTGAAGTGGCAGCTGCCACCGAGCTAGTAAGAGTGTCTGCGCGATGCTT 663
Qy 159 IleGlyPheValSerCysIleSerThrLeuCysIleGlyAlaAlaPheSerTyrTyr 178
Db 664 TTCCTGCTGATCGGCTGCTGCTCTTGTCTCTCACGCCACGCTTCGTGTCTATATG 723
Qy 179 GluArgTrpThrPhePheGlnAlaTyrTyrCysPheIleThrLeuThrThrIleGly 198
Db 724 GAGGACTGGAGCAAGCTGGAGGCCATCTACTTTGTATAGTAGCTTACCACGCTGGGC 783
Qy 199 PheGlyAspTyrValAlaLeuGlnLysAspGlnAlaLeuGlnThrGlnProGlnTyrVal 218
Db 784 TTTGGCGACTATGTGGCGCGCGGACCCAGG-----CAGGACTCCCGCGCTATCAG 837
Qy 219 AlaPheSerPheValTyrIleLeuThrGly-----LeuThrVal 231
Db 838 CCGCTGGTGGTGTCTGGATCTCTGCGGCTGGCTTACTTCGCTCAGTGTCCACCACC 897
Qy 232 IleGlyAlaPheLeuAsnLeuValValLeuArgPheMetThrMetAsnAla----- 248
Db 898 ATCGGGAAGTGGTGGCAGTAGTGTCCCGCGCAGCTCGGCGAGA-GATGGGCGGCTCAC 956
Qy 249 -----GluAspGluLysArgAspAlaGluHisArgAla 259
Db 957 GGCTCAGGCTGCCAGCTGGCAGCTGACAGCGCGCTGACCCAGCAGCGCGGCC 1016
Qy 260 LeuLeuThrHisAsnGlyGlnAlaValGlyLeuGlyLeuSerCysLeuSerGlySer 279
Db 1017 CGCGCGCGCGCGCGAGAGGAGCAGCAGCTGCTGCCCTCCACCGCCCTGTCCAGCGCA 1076
Qy 280 LeuGly-----AspValArgProArgAspProValThrCysAlaAlaAla 294
Db 1077 GCGCTGGGCGAGCGCCCGATCCCTTCGCCCCCGAGAGAGC---TCAGCGGCTTCCCC 1133
Qy 295 AlaGlyGlyValGlyValGlyVal 302
Db 1134 GCCCAGCGCTCGGCCCTGGATTA 1157
```

Search completed: September 16, 2005, 04:40:28

Job time : 304 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 16, 2005, 03:50:28 ; Search time 2209 Seconds
(without alignments)
1221.522 Million cell updates/sec

Title: US-09-939-483-5
Perfect score: 2105
Sequence: 1 ENVRTLALIVCTFYLLVGA.....STGLHSLAARGLMKRRSSV 405

Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 7389322 seqs, 333128599 residues

Total number of hits satisfying chosen parameters: 14778644

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09939483/runat_15092005_111358_9638/app_query.fasta_1.583
-DB-published Applications NA -QFMT=fastap -SUFFIX=rpnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HRAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000 -WMAP=US09939483 @CGN 1 1 810 @runat_15092005_111358_9638
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=10 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq.*
- 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq.*
- 22: /cgn2_6/ptodata/2/pubpna/US10J_NEW_PUB.seq.*
- 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1819	86.4	1551	22	US-10-820-474A-202	Sequence 202, App
2	1819	86.4	2514	9	US-09-939-484-3	Sequence 3, Appli
3	1819	86.4	2514	9	US-09-939-483-3	Sequence 7, Appli
4	1819	86.4	2590	16	US-10-146-733-7	Sequence 4089, Ap
5	1819	86.4	2590	22	US-10-756-149-4089	Sequence 52, Appl
6	1422	67.6	956	8	US-08-816-011-52	Sequence 55, Appl
7	1422	67.6	956	21	US-10-870-492-52	Sequence 2, Appli
8	1326	63.0	854	9	US-09-746-491-55	Sequence 40, Appl
9	1100	52.3	1125	16	US-10-146-733-42	Sequence 56, Appl
10	1100	52.3	1125	9	US-09-798-584-2	Sequence 57, Appl
11	1100	52.3	1248	17	US-10-257-022-21	Sequence 41, Appli
12	1100	52.3	1262	16	US-10-146-733-40	Sequence 6, Appli
13	1100	52.3	2312	9	US-09-798-584-5	Sequence 75, Appl
14	850.5	40.4	1286	9	US-09-746-491-56	Sequence 21, Appl
15	850.5	40.4	1286	9	US-09-746-491-57	Sequence 52, Appl
16	850.5	40.4	1286	17	US-10-173-999-41	Sequence 4, Appli
17	850.5	40.4	1528	16	US-10-146-733-4	Sequence 41, Appli
18	843	40.0	1200	16	US-10-146-733-6	Sequence 6, Appli
19	842.5	40.0	1216	9	US-09-746-491-21	Sequence 21, Appl
20	842.5	40.0	1216	18	US-10-336-472-75	Sequence 1, Appli
21	842.5	40.0	1528	16	US-10-146-733-1	Sequence 75, Appl
22	842.5	40.0	2460	17	US-10-257-022-28	Sequence 28, Appl
C 23	835	39.7	1113	18	US-10-336-472-73	Sequence 73, Appl
C 24	835	39.7	1113	18	US-10-336-472-77	Sequence 77, Appl
C 25	835	39.7	1113	18	US-10-336-472-83	Sequence 83, Appl
C 26	835	39.7	1200	16	US-10-146-733-3	Sequence 3, Appli
C 27	779.5	37.0	1434	22	US-10-450-763-29264	Sequence 29264, A
C 28	721	34.3	766	9	US-09-864-761-17873	Sequence 17873, A
C 29	713.5	33.9	887	20	US-10-363-345A-16137	Sequence 16137, A
C 30	713.5	33.9	887	20	US-10-363-345A-16138	Sequence 16138, A
C 31	713.5	33.9	887	21	US-10-363-483A-16137	Sequence 16137, A
C 32	713.5	33.9	887	21	US-10-363-483A-16138	Sequence 16138, A
C 33	713	33.9	887	20	US-10-363-345A-16139	Sequence 16139, A
C 34	713	33.9	887	20	US-10-363-345A-16140	Sequence 16140, A
C 35	713	33.9	887	21	US-10-363-483A-16139	Sequence 16139, A
C 36	713	33.9	887	21	US-10-363-483A-16140	Sequence 16140, A
C 37	518	24.6	539	18	US-10-074-978A-23	Sequence 23, Appl
C 38	518	24.6	539	18	US-10-424-599-73575	Sequence 73575, A
C 39	462.5	22.0	457	22	US-10-756-149-1478	Sequence 1478, Ap
C 40	369	17.5	2268	21	US-10-461-862-128	Sequence 128, App
C 41	364.5	17.3	879	17	US-10-451-892-9	Sequence 9, Appli
C 42	362.5	17.2	1628	10	US-09-852-386-35	Sequence 35, Appl
C 43	362.5	17.2	2523	21	US-10-461-862-131	Sequence 131, App
C 44	360	17.1	2351	18	US-10-459-190-3	Sequence 3, Appli
C 45	359	17.1	914	17	US-10-451-892-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-10-820-474A-202
; Sequence 202, Application US/10820474A
; Publication No. US2005015089A1
; GENERAL INFORMATION:
; APPLICANT: LAL, PREETI
; APPLICANT: TANG, Y. TOM
; APPLICANT: GORGONE, GINA A.
; APPLICANT: CORLEY, NEIL C.
; APPLICANT: GUEGLER, KARL J.
; APPLICANT: BAUGHN, MARIAH R.
; APPLICANT: AKERBLOM, INGRID E.
; APPLICANT: AU-YOUNG, JANICE
; APPLICANT: YUE, HENRY
; APPLICANT: PATTERSON, CHANDRA
; APPLICANT: REDDY, ROOPA

```

; APPLICANT: HILLMAN, JENNIFER L.
; APPLICANT: BANDMAN, OLGA
; TITLE OF INVENTION: SIGNAL PEPTIDE-CONTAINING MOLECULES
; FILE REFERENCE: 039386-1568
; CURRENT APPLICATION NUMBER: US/10/820,474A
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: 09/720,533
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: PCT/US99/14484
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/090,762
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/094,983
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: 60/102,686
; PRIOR FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 202
; LENGTH: 1551
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte Clone No: 1229438
US-10-820-474A-202

Alignment Scores:
Pred. No.: 2.9e-199 Length: 1551
Score: 1819.00 Matches: 357
Percent Similarity: 90.37% Conservatives: 9
Best Local Similarity: 88.15% Mismatches: 25
Query Match: 86.41% Indels: 14
DB: 22 Gaps: 2

US-09-939-483-5 (1-405) x US-10-820-474A-202 (1-1551)

Qy 1 GluAsnValArgThrLeuAlaLeuIleValCysThrPheThrTyrLeuLeuValGlyAla 20
Db 41 CAGAACGTGGCGACGCTGGGGCTCATCTGTGTGCACCTTACCTTACCTGTGTGGGGGCC 100

Qy 21 AlaValPheAspAlaLeuGluSerGluProGluMetIleGluArgGlnArgLeuGluLeu 40
Db 101 GCGGTCTTCAGCGCGCTGGAGTCGAGCGCCCGAGCTGATGATGAGCGGCGAGCGCTGGAGCTG 160

Qy 41 ArgGlnLeuGluLeuArgAlaAArgTyrAsnLeuSerGluGlyTyrGluLeuGlu 60
Db 161 CGGCAGCAGGAGCTGCGGGCGCGCTACAACTTCAGCCAGGCGGCGCTACGAGGAGCTGGAG 220

Qy 61 ArgValValLeuArgLeuLeuLysProHisLysAlaGlyValGlnTrpArgPheAlaGlySer 80
Db 221 CGGTGTGTGTGGCCCTCAGACCGCCACAGCGCGGCGTGCAGTGGCGCTTCGCGGGCTCC 280

Qy 81 PheTyrPheAlaIleThrValIleThrIleGlyTyrGlyHisAlaAlaProSerThr 100
Db 281 TTCTACTTGGCATCCCGTCATCACCACCATCGCTACGGCGACGCGGCGACCCAGCACG 340

Qy 101 AspGlyLysValPheCysMetPheTyrAlaLeuLeuGlyIleProLeuThrLeuIle 120
Db 341 GATGGCGGCAAGGTGTTCTGCATGTTCTACGCGTGTGGCATCCCGCTCAGCGCTCGTC 400

Qy 121 MetPheGlnSerLeuGlyGluAArgIleAsnThrPheValArgTyrLeuLeuHisArgAla 140
Db 401 ATGTTCCAGAGCTTGGCGGAGCGCATCAACCTTGTGTAGGTACCTGTGCACCGCGCC 460

Qy 141 LysArgGlyLeuGlyMetArgHisAlaGluValSerMetAlaAsnMetValLeuIleGly 160
Db 461 AAGAAGGGCTGGGCATGCGGCGCGCGAGCGTGTCCATGCCAACATGGTGTCTCATCGGC 520

Qy 161 PheValSerCysIleSerThrLeuCysIleGlyAlaAlaAlaPheSerTyrTyrGluArg 180
Db 521 TTCTTCTCGTCATCAGCAGCTGTGCATCGGCGCGCGCTTCTCCCTACAGAGCAC 580

; TrpThrPhePheGlnAlaTyrTyrCysPheIleThrLeuThrThrIleGlyPheGly 200
; TGGACCTTTTCCAGGCCTACTACTACTGTTTCATCACCCTCACCACCATCGGCTTCGGC 640
; AspTyrValAlaLeuGlnLysAspGlnAlaLeuGlnThrGlnProGlnTyrValAlaPhe 220
; GACTACGTGGCGTGCAGAAGGACCAAGGCGCTGCAGACGCGAGCGAGTACGTGGCGCTTC 700
; SerPheValTyrIleLeuThrGlyLeuThrValIleGlyAlaPheLeuLeuValVal 240
; AGCTTCGTCTACATCTTACGGGCTTCACGGTTCATCGGGCGCTTCTCAACCTCTGGTGG 760
; LeuArgPheMetThrMetAsnAlaGluAspGluLysArgAlaAspAlaGluHisArgAlaLeu 260
; CTGCGCTTTCATGACCATGAACGCGGAGGAGAGAGAGCGGCGGAGCGGCGGCTG 820
; LeuThrHisAsnGlyGlnAlaValGlyLeuGlyLeuSerCysLeuSerGlySerLeu 280
; CTCACGCGCAACGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 859
; GlyAspValArgProArgAspProValThrCysAlaAlaAlaGlyGlyValGlyVal 300
; GGCAGCGCGCACACTACGAGCACCGGCTCATCCACGCGGCGGCGGCGGCGGCGGCGG 904
; GlyValGlySerGlyPheArgAsnValTyrAlaGluValLeuHisPheGlnSerMet 320
; GCGGCGGCGGCGGCTTCGCAACGCTTACGCGGAGGCTGTCGACATTCACATCCATG 958
; CysSerCysLeuTrpTyrLysSerArgGluLysLeuGlnTyrSerIleProMetIleIle 340
; TGCTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1018
; ProArgAspLeuSerThrSerAspThrCysValGluHisSerHisSerSerProGlyGly 360
; CGCGGCGGCGGCTTCCACGTCGACGCTGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 1078
; GlyGlyArgTyrSerAspThrProSerHisProCysLeuCysSerGlyThrGlnArgSer 380
; GCGGCGGCGGTACAGCGCACGCGCTTCGCGAGCGGTGCTGTGCGAGCGGCGGCGGCGG 1138
; AlaIleSerSerValSerThrGlyLeuHisSerLeuAlaAlaPheArgGlyLeuMetLys 400
; GCCATCAGCTCGGTGTCCAGCGGTGTGCAGCGCTGTCCACGCTTCCCGCGGCTCATGA 1139
; ArgArgSerSerVal 405
; CGCAGGAGCTCCGTG 1213

RESULT 2
US-09-939-484-3
; Sequence 3, Application US/09939484
; Patent No. US20020032322A1
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Fink, Michel
; APPLICANT: Lazdunski, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; FILE REFERENCE: 1201-CIP-DIV-00
; CURRENT APPLICATION NUMBER: US/09/939,484
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/144,914
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 08/749,816
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: 60/095,234
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: FR 96/01565
; PRIOR FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3

```

	;	LENGTH:	2514	
	;	TYPE:	DNA	
	;	ORGANISM:	Homo sapiens	
	;	FEATURE:		
	;	NAME/KEY:	CDS	
	;	LOCATION:	(126)..(1307)	
	;	OTHER INFORMATION:	TASK	
	;	US-09-939-484-3		
		Alignment Scores:		
	Pred. No.:	5_95e-199	Length:	2514
	Score:	1819.00	Matches:	357
	Percent Similarity:	90.37%	Conservative:	9
	Best Local Similarity:	88.15%	Mismatches:	25
	Query Match:	86.41%	Indels:	14
	DB:	9	Gaps:	2
		US-09-939-483-5 (1-405) x US-09-939-484-3 (1-2514)		
QY	1	GluAsnValArgThrLeuAlaLeuleValCysThrPheThrTyrLeuLeuValGlyAla	20	
DB	135	CAGACGGTCGCACGTGGCGCTCATCGTGTCACCTTTCACTACTGCTGGTGGCGCC	194	
QY	21	AlaValPheAspAlaLeuSerGlnProGluMetIleGluAraGlnArgLeuGluLeu	40	
DB	195	GGCGTCTTCGACGCCGTGGAGTCGAGCCGAGCTGATCGAGCGGCGCACGGCTCGAGCTG	254	
QY	41	ArgGlnLeuGluLeuArgAlaArgTyrrAnLeuSerGluGlyGlyTyrrGluLeuGlu	60	
DB	255	CGCACACGAGCTGGCGCGCGCTACACCTCAGCCAGCGCGGCTGAGAGCTGGAG	314	
QY	61	ArgValValLeuArgLeuLysProHisValAlaGlyValGlnTrpArgPheAlaGlySer	80	
DB	315	CGGTCGTGTCGCCCTCAAGCGGCACAAAGCGCGCGTGCAGTGCGGCTTCGCGGCTCC	374	
QY	81	PheTyrrPheAlaIleThrVallleThrIleGlyTyrrGlyHiseAlaAlaProSerThr	100	
DB	375	TTCTACTTCCCATCACCCTCATCCACCATTCCGCTACGGCGCACGGCGCACCCAGCAGC	434	
QY	101	AspGlyGlyValPheCysMetPheTyrrAlaLeuGlyIleProLeuThrLeuIle	120	
DB	435	GATGGCGGAAGGTFTTGCATGTTCACGGCGTGTGGCGCATCCCCGCTCACGCTCGTC	494	
QY	121	MetPheGlnSerLeuGlyGluArgIleAsnThrPheValArgTyrrLeuLeuHiseArgAla	140	
DB	495	ATGTTCCAGAGCTGGCGCAGCGCATCAACCTTGGTGAGGTACCTGCTGCACCGCGCC	554	
QY	141	LysArgGlyLeuGlyMetArgHiseAlaGluValSerMetAlaAsnMetValLeuIleGly	160	
DB	555	AAGAAGGGCTGGCATGCGCGCGCGCGCTCCATGGCTCATGGCAACATGGTCTCATCGGC	614	
QY	161	PheValSerCysteIseThrLeuCysIleGlyAlaAlaAlaPheSerTyrrGluArg	180	
DB	615	TTCTTCGTGTATCAGCAGCTGTGCATPGCGCGCGCGCTTCTCCCATAAGAGCAGC	674	
QY	181	TriThrPhePheGlnAlaTyrrTyrrCysPheIleThrLeuThrIleGlyPheGly	200	
DB	675	TGGACCTTCTTCAGGCTTACTACTGTTCATCACCCTCACCACTCGGCTTCGGC	734	
QY	201	AspTyrrValAlaLeuGlnLysAspGlnAlaLeuGlnThrGlnProGlnTyrrValAlaPhe	220	
DB	735	GACTAGCTGGCGCTGCAGAAGAACCGAGCCCTGACAGCGCACGCTGGCTTC	794	
QY	221	SerPheValTyrrIleLeuThrGlyLeuthrValIleGlyAlaPheLeuAsnLeuValVal	240	
DB	795	AGCTTCGTCTACATCCCTACGGGCTCATCGGTTCATCGGCGCTTCCTCAACCTCGTGGTG	854	
QY	241	LeuArgPheMetThrMetAsnAlaGluAspGluLysArgAspAlaGluHiseArgAlaLeu	260	
DB	855	CTCGCTTTCATGACCATGTAACCCGAGGACGAGAGCGGAGCGGCGGCGCGCTG	914	
QY	261	LeuThrHiseAsnGlnAlaValGlyLeuGlyLeuSerCysLeuSerGlySerLeu	280	

US-09-939-483-5 (1-405) x US-09-939-483-3 (1-2514)

Alignment Scores:
Pred. No.: 5_95e-199 Length: 2514
Score: 1819.00 Matches: 357
Percent Similarity: 90.37% Conservative: 9
Best Local Similarity: 88.15% Mismatches: 25
Query Match: 86.41% Indels: 14
DB: 9 Gaps: 2

Alignment Scores:

Argument Scores:	6.22e-199	Length:	2590
Pred. No.:	1819.00	Matches:	357
Score:	90.37%	Conservative:	9
Percent Similarity:	88.15%	Mismatches:	25
Best Local Similarity:	86.41%	Indels:	14
Query Match:	16	Gaps:	2
DB:			

US-09-939-483-5 (1-405) x US-10-146-733-7 (1-2590)

Qy	1	GluAsnValArgThrLeuAlaLeuIleValCysThrPheThrTyrLeuLeuValGlyAla	20
Db	135	CGAAACGTGCGACGCTGCGCTCATCTGTGTCACTTCACTTACCTTGTGTGTGGCGCC	194
Qy	21	AlaValPheAspAlaLeuGluSerGluProGluMetIleGluArgGlnArgLeuGluLeu	40
Db	195	GGGGTCTTCGACGCGCTGGAGTCGGAGCCCGAGCTGATCGAGCGGACCGCGCTGGAGCTG	254
Qy	41	ArgGlnLeuGluLeuArgAlaArgTyrAsnLeuSerGluGlyGlyTyrGluGluLeuGlu	60
Db	255	CGGACGACGAGACTGCGGGCGCTACAACTCATGCCAGGGCGGTACGAGGAGCTGGAG	314
Qy	61	ArgValValLeuArgLeuLysProHisLysAlaGlyValGlnTrpArgPheAlaGlySer	80
Db	315	CGCGTCGTCTCGCTCAAGCCGCACAAAGCCGCGTGCAGTGGCGCTTCGCGCGCTCC	374
Qy	81	PheTyrPheAlaIleThrValIleThrThrIleGlyTyrGlyHisAlaAlaProSerThr	100
Db	375	TTCTACTTCGCCCATCACCCTCATCACCACTCGGTACGGGCACGCGGCACCCAGCACG	434
Qy	101	AspGlyGlyLysValPheCysMetPheTyrAlaLeuLeuGlyIleProLeuThrLeuIle	120
Db	435	GATGGCGGCAAGGTGTTCTGATGTTCTACCGCGTGTCTGGGCATCCCGCTCAGCTCGTC	494
Qy	121	MetPheGlnSerLeuGlyGluArgIleAsnThrPheValArgTyrLeuLeuHisArgAla	140
Db	495	ATGTTCCAGAGCCTGGGCGAGCGCATCAACACTTGTGTAGGTACTGTCTGCACCGCGCC	554
Qy	141	LysArgGlyLeuGlyMetArgHisAlaGluValSerMetAlaAsnMetValLeuIleGly	160
Db	555	AAGAAGGGCTGGGCATCGCGCGCGCGACGTCTCCATGGCCAACTGGTGTCTCATCGGC	614
Qy	161	PheValSerCysIleSerThrLeuCysIleGlyAlaAlaPheSerTyrTyrGluArg	180
Db	615	TTCTTCTCGTCATCAGCACGCTGTGTGATCTCGCGCGCGCTTCTCCCACTCAGAGCAC	674
Qy	181	TrpThrPhePheGlnAlaTyrTyrCysPheIleThrLeuThrThrIleGlyPheGly	200
Db	675	TGGACCTCTTCCAGCGCTACTACTACTGCTTCTCATCCCTCACCACTCGGCTTCGGC	734
Qy	201	AspTyrValAlaLeuGlnLysAspGlnAlaLeuGlnThrGlnProGlnTyrValAlaPhe	220
Db	735	GACTAGTGGCGCTGCAAGGACGAGGCCCTTCGACGCGACGCGCTAGTGGCTTC	794
Qy	221	SerPheValTyrIleLeuThrGlyLeuThrValIleGlyAlaPheLeuAsnLeuValVal	240
Db	795	AGCTTCGTCTACATCTTACGGGCTCACGGTCTCATCGCGCTTCTCAACCTCGTGGTG	854
Qy	241	LeuArgPheMetThrMetAsnAlaGluAspGluLysArgAspAlaGluHisArgAlaLeu	260
Db	855	CTCGCGTTCATGACCATGAACCCGAGGACGAGAGCGCGACGCGCGAGCACCGCGCGCTG	914
Qy	261	LeuThrHisAsnGlyGlnAlaValGlyLeuGlyGlyLeuSerCysLeuSerGlySerLeu	280
Db	915	CTCAGCGGCAACGGGCGGCGCGCGCGCGGAGGG	953
Qy	281	GlyAspValArgProArgAspProValThrCysAlaAlaAlaIleGlyValGlyVal	300
Db	954	GGCAGCGCCACACTACGGACACCGCCTCATCCAGCGGCGGAGG	998
Qy	301	GlyValGlyLysGlyPheArgAsnValTyrAlaGluValLeuHisPheGlnSerMet	320

```
Db 435 GATGGCGCAAGGTGTTCTGCATCTTACGCGCTGTGGCATCCCGCTCACGCTCGTC 494
Qy 121 MetPheGlnSerLeuGluArgGluAsnThrPheValArgTyrLeuLeuHisArgAla 140
Db 495 ATGTTCCAGAGCCCTGGGCGAGCGCATCAACACCTTGGTGAGGTACCTGCTGCACCGCGCC 554
Qy 141 LysArgGlyLeuGlyMetArgHisAlaGluValSerMetAlaAsnMetValLeuLeuGly 160
Db 555 AAGAAGGGCTGGCATGCGCGCGCGCATGTCATGGCCACATGGTGCTCATCGGC 614
Qy 161 PheValSerCysIleSerThrLeuCysIleGlyAlaAlaPheSerTyrTyrGluArg 180
Db 615 TTCTTCTCGTCATCAGCAGCTGTGCATCGCGCGCGCTTCTCCCACTACGAGCAC 674
Qy 181 TrpThrPhePheGlnAlaTyrTyrCysPheIleThrLeuThrThrIleGlyPheGly 200
Db 675 TGGACCTTCTTCCAGGGCTTACTACTGTCTTCAACCTCACCACTCGGCTCGGC 734
Qy 201 AspTyrValAlaLeuGlnLysAspGlnAlaLeuGlnThrGlnProGlnTyrValAlaPhe 220
Db 735 GACTACGTGGCGCTGCAGAGGACCGAGCCCTGCAGACGCGAGCTAGTGGCCTTC 794
Qy 221 SerPheValTyrIleLeuThrGlyLeuThrValIleGlyAlaPheLeuAsnLeuValVal 240
Db 795 AGCTTCGTCTACATCCTTACGGGCTCACGCTCATCGCGCTTCTCAACCTCGTGCTG 854
Qy 241 LeuArgPheMetThrMetAsnAlaGluAspGluLysArgAspAlaGluHisArgAlaLeu 260
Db 855 CTGCGCTTCATGACCATGAAGCGCGAGGAGAGAGCGAGCGCGAGCGCGCGCGCTG 914
Qy 261 LeuThrHisAsnGlyGlnAlaValGlyLeuGlyLeuSerCysLeuSerGlySerLeu 280
Db 915 CTCACGCGCAACGGCGAGCGCGCGCGCGGAGGG-----GGT 953
Qy 281 GlyAspValArgProArgAspProValThrCysAlaAlaAlaGlyValGlyVal 300
Db 954 GGCAGCGCGCACACTACGGACACCGCCCTCATCCACGCGCGCAGCG----- 998
Qy 301 GlyValGlyGlySerGlyPheArgAsnValTyrAlaGluValLeuHisPheGlnSerMet 320
Db 999 -----GGCGCGCGCGCTCCGCAACGCTACGCGGAGGTGTGCACCTTCCAGTCCATG 1052
Qy 321 CysSerCysLeuTyrTyrLysSerArgGluLysLeuGlnTyrSerIleProMetIleIle 340
Db 1053 TGCTCGTCTGTGTACAGAGCGCGAGAGCTGCAGTACTCCATCCCATCATCATC 1112
Qy 341 ProArgAspLeuSerThrSerAspThrCysValGluHisSerHisSerProGlyGly 360
Db 1113 CCGCGGACCTCTCCAGCTCCGACACGCTGGGTGGAGCAGAGCCACTCGTCCGCGGAGGG 1172
Qy 361 GlyGlyArgTyrSerAspThrProSerHisProCysLeuCysSerGlyThrGlnArgSer 380
Db 1173 GGCGGCGCTACAGCAGACGCGCTCGCGAGCTGTGCGAGCGGGGCGCCACGCTCC 1232
Qy 381 AlaIleSerValSerThrGlyLeuHisSerLeuAlaAlaPheArgGlyLeuMetLys 400
Db 1233 GCCATAGCTCGGTGCCAGGGTCTGCACAGCCTGTCCACCTTCCGCGGCTCATGAG 1292
Qy 401 ArgArgSerSerVal 405
Db 1293 CGCAGGAGCTCCGCTG 1307
```

RESULT 6

```
US-08-816-011-52
; Sequence 52, Application US/08816011
; Publication NO. US20030165806A1
; GENERAL INFORMATION:
; APPLICANT: Price, Laura A.
; APPLICANT: Pausch, Mark H.
; TITLE OF INVENTION: Potassium Channels, Nucleotide Sequences
; TITLE OF INVENTION: Encoding Them, and Methods of Using Same
; NUMBER OF SEQUENCES: 56
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Home Products Corporation
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,011
; FILING DATE: 11-MAR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthews, Gale F.
; REGISTRATION NUMBER: 32,269
; REFERENCE/DOCKET NUMBER: 32,421-C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-683-2134
; TELEFAX: 201-683-4117
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 956 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-816-011-52
```

```
Alignment Scores:
Pred. No.: 1 03e-153 Length: 956
Score: 1422.00 Matches: 290
Percent Similarity: 98.31% Conservative: 1
Best Local Similarity: 97.97% Mismatches: 4
Query Match: 67.55% Indels: 4
DB: 8 Gaps: 1
```

US-09-939-483-5 (1-405) x US-08-816-011-52 (1-956)

```
Qy 1 GluAsnValArgThrLeuAlaLeuIleValCysThrPheThrTyrLeuLeuValGlyAla 20
Db 66 GAGAAATGTGCGCAGCTGGCTCTCATCGTGTGCACCTTACCTTACCTGTGTGGTGGCGCC 125
Qy 21 AlaValPheAspAlaLeuGluSerGluProGluMetIleGluArgGlnArgLeuLeu 40
Db 126 GCGGTGTTCGACGCACTGGAGTCGGAGCGCGAGATGATCGAGCGCGAGGCTG 185
Qy 41 ArgGlnLeuGluLeuArgAlaArgTyrAsnLeuSerGluGlyTyrGluGluLeuGlu 60
Db 186 CGGCACCTGGAGCTGGCGGCGCGCTACACCTCAGCGAGGGCGGCTACGAGGAGCTGGAG 245
Qy 61 ArgValValLeuArgLeuLysProHisLysAlaGlyValGlnTrpArgPheAlaGlySer 80
Db 246 CGCGTGTGTGCGCCCTCAAGCGCGCACAAAGCGCGGTGCGAGTGGCGCTTCGCGCGCTCC 305
Qy 81 PheTyrPheAlaIleThrValIleThrThrIleGlyTyrGlyHisAlaAlaProSerThr 100
Db 306 TTCTACTTCGCCATCACCGCTCATCACCATCGGTATGGTATGCGGCGCCAGCAGC 365
Qy 101 AspGlyGlyLysValPheCysMetPheTyrAlaLeuLeuGlyIleProLeuThrLeuIle 120
Db 366 GACGAGGGCAAGGTGTTCTGCATGTTCTACGCGCTCTGGGCATCCCGCTCACACTAGTC 425
Qy 121 MetPheGlnSerLeuGlyGluArgIleAsnThrPheValArgTyrLeuLeuHisArgAla 140
Db 426 ATGTTCCAGAGCCTGGGTGAAAGCATCAACACCTCCGTCGAGGTACCTGTGTGCACCGTCC 485
Qy 141 LysArgGlyLeuGlyMetArgHisAlaGluValSerMetAlaAsnMetValLeuLeuGly 160
Db 486 AAGAGGGGGCTGGGCATGCGGACGCGACCGCAAGTGTCTCATGCCCAACAATGGTCTCATCGGT 545
```


Qy 161 PheValSerCysIleSerThrIleuCysIleGlyAlaAlaAlaPheSerTyrTyrGluArg 180
Db 546 TTCGGTTCGTGCATCAGACCGCTGTGCATCGCGCAGCTGCTTCTCCTACTACGAGCGC 605
Qy 181 TrpThrPhePheGlnAlaTyrTyrCysPheIleThrLeuThrThrIleGlyPheGly 200
Db 606 TGGACTTCTTCCAGGCCATTACTACTGCTTCTCATCCCTCACCACCATCGGCTTGGC 665
Qy 201 AspTyrValAlaLeuGlnLysAspGlnAlaLeuGlnThrGlnProGlnTyrValAlaPhe 220
Db 666 GACTATGTGGCGCTGCAGAGGACCGAGCGCTGCAGACGCGCGCATGTGTGC-TTC 724
Qy 221 SerPheValTyrIleLeuThrGlyLeuThrValIleGlyAlaPheLeuAsnLeuValVal 240
Db 725 AGCTTCGGTGTACATCCTCAGCGGCTC-ACGGTTCATCGCGC-TTCCTCAACCTCGTGGTG 782
Qy 241 LeuArgPheMetThrMetAsnAlaGluAspGluLysArgAspAlaGluHisArgAlaLeu 260
Db 783 CTGGATTTCATGACCATGAACCGGAGGACGAGAGCGTGTATGGGAGCACCGCGCCCTG 842
Qy 261 LeuThrHisAsnGlyGlnAlaValGlyLeuGlyLeuSerCysLeuSerGlySerIleu 280
Db 843 CTCACGACAAACGGCAGCGCTGTGGCTGGGTGGCTGAGCTGCCTGAGCGGTAGCCTG 902
Qy 281 GlyAsp---ValArgProArgAspProValThrCysAlaAlaAlaAla 295
Db 903 GCGACGCGCTGCGTCCCGCGACCCAGTCATGCATGCGCTGCGCGCGCA 950

RESULT 7

US-10-870-492-52
; Sequence 52, Application US/10870492
; Publication No. US20050032165A1
; GENERAL INFORMATION:
; APPLICANT: PAUSCH, MARK H.
; TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
; AND METHODS OF USING SAME
; FILE REFERENCE: 01142.0114 SEQUENCE LISTING
; CURRENT APPLICATION NUMBER: US/10/870,492
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US/09/503,849
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/816,011
; PRIOR FILING DATE: 1997-03-11
; PRIOR APPLICATION NUMBER: PCT/US95/14364
; PRIOR FILING DATE: 1995-10-25
; PRIOR APPLICATION NUMBER: 07/332,312
; PRIOR FILING DATE: 1994-10-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 956
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-870-492-52

Alignment Scores:

Pred. No.: 1.03e-153 Length: 956
Score: 1422.00 Matches: 290
Percent Similarity: 98.31% Conservative: 1
Best Local Similarity: 97.97% Mismatches: 4
Query Match: 67.55% Indels: 4
DB: 21 Gaps: 1

US-09-939-483-5 (1-405) x US-10-870-492-52 (1-956)

Qy 1 GluAsnValArgThrLeuAlaIleValCysThrPheThrTyrLeuLeuValGlyAla 20
Db 66 GAGAAATGGCGACCGTGGCTCTCATCGTGCACCTTACCTGCTGCTGGCGGCC 125
Qy 21 AlaValPheAspAlaLeuGluSerGluProGluMetIleGluArgGlnArgLeuGluLeu 40
Db 126 CGGTGTTCGACGACACTGGAGTGGAGCCGAGATGATCGAGCGCGAGCTGGAGCTG 185

Qy 41 ArgGlnLeuGlnIleuArgAlaArgTyrAsnLeuSerGluGlyTyrGluLeuGluGlu 60
Db 186 CGGCAGCTGGAGCTGCGGGCGCGCTACAACCTCAGCGAGGGCGCTACGAGGAGCTGGAG 245
Qy 61 ArgValValLeuArgLeuLysProHisLeuAlaGlyValGlnTyrArgPheAlaGlySer 80
Db 246 CGGTGTGTGTGGCCCTCAAGCCGACAGCGCGCGGTGAGTGGCGCTTCCGCGGCTCC 305
Qy 81 PheTyrPheAlaIleThrValIleThrThrIleGlyTyrGlyHisAlaAlaProSerThr 100
Db 306 TTCTACTTCGCCATCACCCTCATCCACCATCGGCTATGGTCATGCGGCGCCAGCACG 365
Qy 101 AspGlyLysValPheCysMetPheTyrAlaLeuLeuGlyIleProLeuThrLeuIle 120
Db 366 GACGAGGCGAAGGTGTTCTGCATGTTCTACGCGCTGCTGGGCAATCCCGCTCACACTAGTC 425
Qy 121 MetPheGlnSerLeuGlyGluArgIleAsnThrPheValArgTyrLeuLeuHisArgAla 140
Db 426 ATGTTCCAGAGCCTGGGTGAACGATCAACCTCCGTGAGGTACCTGCTGCACCGTGC 485
Qy 141 LysArgGlyLeuGlyMetArgHisAlaGluValSerMetAlaAsnMetValLeuIleGly 160
Db 486 AAGAGGGGGCTGGGCATGCGGCACGCGAAGTGTCCATGCGCAACATGGTGTCTCATCGGT 545
Qy 161 PheValSerCysIleSerThrLeuCysIleGlyAlaAlaAlaPheSerTyrTyrGluArg 180
Db 546 TTCGTGTGTGCATCAGACGCTGTGCATCGCGCAGCTGCTTCTCTACTACGAGCGC 605
Qy 181 TrpThrPheGlnAlaTyrTyrCysPheIleThrLeuThrThrIleGlyPheGly 200
Db 606 TGGACTTCTTCCAGGCCATTACTGCTTCTATCACCCTCACCATCGGCTTCCGCG 665
Qy 201 AspTyrValAlaLeuGlnLysAspGlnAlaLeuGlnThrGlnProGlnTyrValAlaPhe 220
Db 666 GACTATGTGGCGCTGCAGAGGACCGAGCGCTGCAGACGCGCGCATGTGTGC-TTC 724
Qy 221 SerPheValTyrIleLeuThrGlyLeuThrValIleGlyAlaPheLeuAsnLeuValVal 240
Db 725 AGCTTCGTGTACATCCTCAGCGGCTC-ACGGTTCATCGCGC-TTCCTCAACCTCGTGGTG 782
Qy 241 LeuArgPheMetThrMetAsnAlaGluAspGluLysArgAspAlaGluHisArgAlaLeu 260
Db 783 CTGGATTTCATGACCATGAACCGGAGGACGAGAGCGTGTATGGGAGCACCGCGCCCTG 842
Qy 261 LeuThrHisAsnGlyGlnAlaValGlyLeuGlyLeuSerCysLeuSerGlySerLeu 280
Db 843 CTCACGACAAACGGCAGCGCTGTGGCTGGGTGGCTGAGCTGCCTGAGCGGTAGCCTG 902
Qy 281 GlyAsp---ValArgProArgAspProValThrCysAlaAlaAlaAla 295
Db 903 GCGACGCGCTGCGTCCCGCGACCCAGTCATGCATGCGCTGCGCGCGCA 950

RESULT 8

US-09-746-491-55
; Sequence 55, Application US/09746491
; Patent No. US20020137202A1
; GENERAL INFORMATION:
; APPLICANT: Burgeess, Catherine E.
; TITLE OF INVENTION: No. US20020137202A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-621
; CURRENT APPLICATION NUMBER: US/09/746,491
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: USSN 60/171,329
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 854
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-746-491-55
Alignment Scores:

Pred. No.: 1.07e-142 Length: 854
Score: 1326.00 Matches: 257
Percent Similarity: 97.06% Conservative: 7
Best Local Similarity: 94.49% Mismatches: 8
Query Match: 62.99% Indels: 0
DB: 9 Gaps: 0

US-09-939-483-5 (1-405) x US-09-746-491-55 (1-854)

Qy 1 GluAsnValArgThrLeuAlaLeuValCysThrPheThrTyrLeuLeuValGlyAla 20
Db 10 CAGAACGTGGCGCAGCGTGGCGCTCATCGTGGACCTTCACTACCTGCTGGTGGCGCC 69
Qy 21 AlaValPheAspAlaLeuGluSerGluProGluMetIleGluArgGlnArgLeuGluLeu 40
Db 70 GCGGTCTTCGACGCGCTGGAGTCGAGCGCCGAGCTGATCGAGCGCGCGCTGGAGCTG 129
Qy 41 ArgGlnLeuGluLeuArgAlaArgTyrAsnLeuSerGluGlyTyrGluGluLeuGlu 60
Db 130 CGGCAGCAGGAGCTGCGCGCGCGCTACAACCTCAGCCAGCGCGCTACGAGGAGCTGGAG 189
Qy 61 ArgValValLeuArgLeuLysProHisLysAlaGlyValGlnTrpArgPheAlaGlySer 80
Db 190 CGCGTCGTGCTGCCCTCAAGCCGACCAAGCGCGCGCTGAGTGGCGCTTCGCGCGCTCC 249
Qy 81 PheTyrPheAlaIleThrValIleThrThrIleGlyTyrGlyHisAlaAlaProSerThr 100
Db 250 TTCTACTTCGCGCATCAGCGTCATCCACCATCGGTACGGGCAGCGGCACCGACG 309
Qy 101 AspGlyGlyLysValPheCysMetPheTyrAlaLeuLeuGlyIleProLeuThrLeuIle 120
Db 310 GATGGCGCAAGGTGTTCTGTCATGTTACGCGCTGCTGGGCATCCCGCTCACGCTCGTC 369
Qy 121 MetPheGlnSerLeuGlyGluArgIleAsnThrPheValArgTyrLeuLeuHisArgAla 140
Db 370 ATGTTTCAGAGCCTGGCGGAGCGCATCAACACCTTGTGTGAGGTACCTGTCACCGCGCC 429
Qy 141 LysArgGlyLeuGlyMetArgHisAlaGluValSerMetAlaAsnMetValLeuIleGly 160
Db 430 AAGAAGGGCTGGCATGCGCGCGCGCGCATGCTTCATGGCCACATGGTGTCTCATCGGC 489
Qy 161 PheValSerCysIleSerThrLeuCysIleGlyAlaAlaPheSerTyrTyrGluArg 180
Db 490 TTCTTCTCGTCATCAGCAGCGCTGTGCATCGCGCGCGCGCTTCTCCCACTACGAGCAC 549
Qy 181 TrpThrPheGlnAlaTyrTyrTyrCysPheIleThrLeuThrThrIleGlyPheGly 200
Db 550 TGGACCTTCTTCCAGGCGCTACTACTGTCTTCATCACCCCTCACCATCGGCTTCGGC 609
Qy 201 AspTyrValAlaLeuGlnLysAspGlnAlaLeuGlnThrGlnProGlnTyrValAlaPhe 220
Db 610 GACTACGTGGCGCTGCAGAGGAGCAGCGCTCGAGACGCGAGCGAGTACGTGGCGCTTC 669
Qy 221 SerPheValTyrIleLeuThrGlyLeuThrValIleGlyAlaPheLeuAsnLeuValVal 240
Db 670 AGCTTCGTCTACATCTTACGGGCTCAGCGCTCATCGCGCTTCTCTCAACCTCGTGGTG 729
Qy 241 LeuArgPheMetThrMetAsnAlaGluAspGluLysArgAspAlaGluHisArgAlaLeu 260
Db 730 CTGGCGCTTACATGACATGAACCGCGAGGAGGAGGAGCGAGCGCGAGCACCGCGCGCTG 789
Qy 261 LeuThrHisAsnGlyGlnAlaValGlyLeuGly 272
Db 790 CTCACGGCAACGGCGAGGCGGCGCGCGGAGGG 825

RESULT 9

US-10-146-733-42
; Sequence 42, Application US/10146733
; Publication No. US20030165891A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Silos-Santiago, Inmaculada

Qy 1 GluAsnValArgThrLeuAlaLeuValCysThrPheThrTyrLeuLeuValGlyAla 20
Db 10 CAGAACGTGGGAGCTCTGCTCCCTCATCGTCCCTTACCTTACCTGCTGGTGGCGCC 69
Qy 21 AlaValPheAspAlaLeuGluSerGluProGluMetIleGluArgGlnArgLeuGluLeu 40
Db 21 AlaValPheAspAlaLeuGluSerGluProGluMetIleGluArgGlnArgLeuGluLeu 40

; TITLE OF INVENTION: NOVEL TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615,
; TITLE OF INVENTION: HNDA-1, TWIK-9, alpha3delta-4, 54414, AND 53763 MOLECULES
; FILE REFERENCE: WNI-248
; CURRENT APPLICATION NUMBER: US/10/146,733
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/185,938
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 09/515,520
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 09/518,866
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: US 60/195,734
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US 60/195,993
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: US 60/199,799
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: US 60/233,537
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: US 60/235,018
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 60/235,059
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 60/256,240
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/256,588
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/258,028
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: US 09/796,720
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/828,035
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 09/833,081
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 09/843,128
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/957,683
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: US 09/964,252
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 09/964,256
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 10/024,623
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42

LENGTH: 1122
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1122)
US-10-146-733-42

Alignment Scores:
Pred. No.: 2.06e-116 Length: 1122
Score: 1100.00 Matches: 229
Percent Similarity: 67.07% Conservative: 48
Best Local Similarity: 55.45% Mismatches: 86
Query Match: 52.26% Indels: 50
DB: 16 Gaps: 5

US-09-939-483-5 (1-405) x US-10-146-733-42 (1-1122)


```
Db 490 TTCTTCTCTCGATGGGACCGCTGCGATCGGGCGCGCTTCTCCACGTGTGAGGAG 549
Qy 181 TrpThrPheGlnAlaTyrTyrCysPheIleThrLeuThrThrIleGlyPheGly 200
Db 550 TGGAGCTTCTCCAGCGCTACTACTGCTTTCATCAGTTTGATACATTGGGTTCGGG 609
Qy 201 AspTyrValAlaLeuGlnLysAspGlnAlaLeuGlnThrGlnProGlnTyrValAlaPhe 220
Db 610 GACTACGTGGCCCTGCAGACCAAGGGTGCCCTGCAGAAAGACCGCTCTACGTGGCCTTT 669
Qy 221 SerPheValTyrIleLeuThrGlyLeuThrValIleGlyAlaPheLeuAsnLeuValVal 240
Db 670 AGCTTTATATATCTCTGGTGGCGCTGACGGTCTATCGGGCTTCTCTCAACCTGGTCGTC 729
Qy 241 LeuArgPheMetThrMetAsnAlaGluAspGluLysArgAspAlaGluHisArgAlaLeu 260
Db 730 CTCAGGTTCTTGACCATGAACGTGAGATAGCGGGGATGCTGAAGAGAGGGCATCC 789
Qy 261 LeuThrHisAsnGlyGlnAlaValGlyLeuGlyLeuSerCysLeuSerGlySerLeu 280
Db 790 CTCGCGGAAACCGCAAC-----AGCATGGTCATTCACATCCCT 828
Qy 281 GlyAspValArgProArgAspProValThrCysAlaAlaAlaGlyGlyValGlyVal 300
Db 829 GAGGAGCGCGCGCCGCGGCC----- 852
Qy 301 GlyValGlyGlySerGlyPheArgAsnValTyrAlaGluValLeuHisPheGlnSerMet 320
Db 853 -----AGGTACAGCGCGGACGTCCCGGACCTGCGACTCTGTG 888
Qy 321 CysSerCysLeuTrpTyrLysSerArgGluLysLeuGlnTyrSerIleProMetIleIle 340
Db 889 TGCTCCTGCACCTGCTACCGCTCGCAGGAC-----TATGCGCGCGCTCGGTGGCA 939
Qy 341 ProArgAspLeuSerThrSerAspThrCysValGluHisSerHisSer----- 356
Db 940 CCGCAGAACTCTCTTCAGCGGCAAGCTTGCCCGCCACTACTTCCACTCCATCTCTTACAAG 999
Qy 357 -----SerProGlyGlyGlyArgTyrSerAspThrProSerHisProCys 372
Db 1000 ATCCAGAGATCTCCACNAGC-----ACA 1023
Qy 373 LeuCysSerGlyThrGlnArgSerAlaIleSerSerValSerThrGlyLeuHisSerLeu 392
Db 1024 TTAATAAACACGCTCTTCCCATCGCTATTAGCTCCATCTCTCTCGGTTTACAGACTTT 1083
Qy 393 AlalaPheArgGlyLeuMetLysArgSerSerVal 405
Db 1084 ACCGACCACCAAGGCTGATGAACCGCGGAAGTCGGTT 1122

RESULT 11
US-10-257-022-21
; Sequence 21, Application US/10257022
; Publication No. US20030211499A1
; GENERAL INFORMATION:
; APPLICANT: REDDY, Roopa
; APPLICANT: THORNTON, Michael
; APPLICANT: BOROWSKY, Mark L.
; APPLICANT: TANG, Y. Tom
; APPLICANT: KHAN, Farrah A.
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: YAO, Monique G.
; APPLICANT: SANJANWALA, Madhusudan M.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: NGUYEN, Dannel B.
; APPLICANT: POLICKY, Jennifer L.
; APPLICANT: YUE, Henry
; APPLICANT: SEITHAMER, Jeffrey J.
; APPLICANT: WALIA, Narinder K.
; APPLICANT: LAL, Preeti
; APPLICANT: KEARNEY, Liam
; APPLICANT: WALSH, Roderick T.
```

```
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: LU, Yan
; APPLICANT: GREENE, Barrie D.
; APPLICANT: RAUMANN, Brigitte E.
; APPLICANT: Arvizu, Chandra S.
; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
; FILE REFERENCE: PI-0067 USN
; CURRENT APPLICATION NUMBER: US/10/257,022
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: US01/11206
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/195,595
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/196,872
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/199,020
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/200,552
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/202,348
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/203,495
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PERL Program
```

```
; SEQ ID NO 21
```

```
; LENGTH: 1248
```

```
; TYPE: DNA
```

```
; ORGANISM: Homo sapiens
```

```
; FEATURE:
```

```
; NAME/KEY: misc feature
```

```
; OTHER INFORMATION: Incyte ID No: 7472584CB1
```

```
US-10-257-022-21
```

```
Alignment Scores:
```

Pred. No.:	2,41e-116	Length:	1248
Score:	1100.00	Matches:	229
Percent Similarity:	67.07%	Conservative:	48
Best Local Similarity:	55.45%	Mismatches:	86
Query Match:	52.26%	Indels:	50
DB:	17	Gaps:	5

```
US-09-939-483-5 (1-405) x US-10-257-022-21 (1-1248)
```

```
Qy 1 GluAsnValArgThrLeuAlaLeuIleValCysThrPheThrTyrLeuLeuValGlyVala 20
```

```
Db 10 CAGAACGTGGGACTCTGTCCTCATCGCTTCACCTTCACCTGCTGGTGGGGCGCC 69
```

```
Qy 21 AlaValPheAspAlaLeuGluSerGluProGluMetIleGluArgGlnArgLeuGluLeu 40
```

```
Db 70 GCGGTGTCGACGCCCTCGAGTCGGACCAAGATGCGGAGGAGGAGAACTCAAAGCC 129
```

```
Qy 41 ArgGlnLeuGluLeuArgAlaArgTyrAsnLeuSerGluGlyTyrGluGluLeuGlu 60
```

```
Db 130 GAGGAGATCCGATCAAGGGGAAGTACAACATCAGCAGCGAGGACTACCGGCAGCTGGAG 189
```

```
Qy 61 ArgValValLeuArgLeuLysProHisLysAlaGlyValGlnTrpArgPheAlaGlySer 80
```

```
Db 190 CTGGTGATCTCGAGTCGGAACCGCGCGCGCGCTCAGTGGAAATTCGCCGGCTCC 249
```

```
Qy 81 PheTyrPheAlaIleThrValIleThrIleGlyTyrGlyHisAlaAlaProSerThr 100
```

```
Db 250 TTCTACTTTGGGATCAGCGTCAACCAACCATAGATTATGGGCACGCTGCACCTGGCACC 309
```

```
Qy 101 AspGlyGlyLysValPheCysMetPheTyrAlaLeuLeuGlyTyrProLeuThrLeuIle 120
```

```
Db 310 GATCGCGCAAGGCCCTTCTGCATGTTCTACGCGCGCTCGGGCATCTCCGCTGACACTGGTC 369
```

```
Qy 121 MetPheGlnSerLeuGlyGluArgIleAsnThrPheValArgTyrLeuLeuHisArgAla 140
```

```
Db 370 ATGTTCCAGACCTGGCGGAGCGGCAACACCTTCGTCGGCTTACCTGCTGAAGCGCATTT 429
```

```
Qy 141 LysArgGlyLeuGlyMetArgHisAlaGluValSerMetAlaAsnMetValLeuIleGly 160
```

```
Db 430 AAGAAGTCTGTGGCATGCGCAACTGACGGTCTATGGAGAAATCATGGTGAAGTGTGGC 489
Qy 161 PheValSerCysIleSerThrLeuCysIleGlyAlaAlaAlaPheSerTyrTyrGluArg 180
Db 490 TTCTTCTCTGTCATGGGAGCGTGTGCATCGGGCGCGCTTCTCCAGTGTGAGGAG 549
Qy 181 TrpThrPhePheGlnAlaTyrTyrCysPheIleThrLeuThrThrIleGlyPheGly 200
Db 550 TGGAGCTTCTTCCAGCGCTACTACTGCTTCTCATCAGCTTGCATACCACTGGGTTCGGG 609
Qy 201 AspTyrValAlaLeuGlnLysAspGlnAlaLeuGlnThrGlnProGlnTyrValAlaPhe 220
Db 610 GACTACGTGGCCCTGCAGACCAGGGTGCCTGCAGAAAGAGCCGCTCTACGTGGCCCTTT 669
Qy 221 SerPheValTyrIleLeuThrGlyLeuThrValIleGlyAlaPheLeuAsnLeuValVal 240
Db 670 AGCTTTATGATATCTCGTGGGGCTGACGGTTCATCGGGCGCTTCTCAACCTGGTCTGC 729
Qy 241 LeuArgPheMetThrMetAsnAlaGluAspGluLysArgAspAlaGluHisArgAlaLeu 260
Db 730 CTCAGGTCTTTCACCATCAACAGTGAAGTGAAGCGCGGATGCTGAAGAGAGGCGCATCC 789
Qy 261 LeuThrHisAsnGlyGlnAlaValGlyLeuGlyGlyLeuSerCysLeuSerGlySerLeu 280
Db 790 CTCGCGCGAAACCGCAAC-----AGCATGGTCACTTCCATCCATCCCT 828
Qy 281 GlyAspValArgProArgAspProValThrCysAlaAlaAlaAlaGlyValGlyVal 300
Db 829 GAGGAGCGCGGCCCGCGGCC-----852
Qy 301 GlyValGlyGlySerGlyPheArgAsnValTyrAlaGluValLeuHisPheGlnSerMet 320
Db 853 -----AGGTACAAGCGCGACGCTCCCGGACCTCGCAGTCTGTG 888
Qy 321 CysSerCysLeuTrpTyrLysSerArgGluLysLeuGlnTyrSerIleProMetIleIle 340
Db 889 TGCTCTCGACCTGCTACCGCTCGCAGGAC-----TATGGCGCGCGCTCGGTGGCA 939
Qy 341 ProArgAspLeuSerThrSerAspThrCysValGluHisSerHisSer-----356
Db 940 CGCAGAACTCTTTCAGCGCCCAAGCTTCCCGCCCACTACTTCCATCTCTTACAAAG 999
Qy 357 -----SerProGlyGlyGlyGlyArgTyrSerAspThrProSerHisProCys 372
Db 1000 ATCAGGAGAGATCTCACCAGC-----ACA 1023
Qy 373 LeuCysSerGlyThrGlnArgSerAlaIleSerSerValSerThrGlyLeuHisSerLeu 392
Db 1024 TTAATAAAACAGCCTCTCCCATCGCTATTAGCTCCATCTCTCTGGGTATACAGCTTT 1083
Qy 393 AlaAlaPheArgGlyLeuMetLysArgArgSerSerVal 405
Db 1084 ACCGACACACAGAGGCTGATGNAACCGCGGAATCCGTT 1122

RESULT 12
US-10-146-733-40
; Sequence 40, Application US/10146733
; Publication No. US20030165891A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Glucksmann, Maria A.
; TITLE OF INVENTION: NOVEL TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615.
; TITLE OF INVENTION: HMMDA-1, TWIK-9, alpha2delta-4, 54414, AND 53763 MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: MN1-248
; CURRENT APPLICATION NUMBER: US/10/146,733
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/185,938
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 09/515,520
; PRIOR FILING DATE: 2000-02-29
```

```
; PRIOR APPLICATION NUMBER: US 09/518,866
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: US 60/195,734
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US 60/195,993
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: US 60/199,799
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: US 60/233,537
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: US 60/235,018
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 60/235,059
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 60/256,240
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/256,588
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/258,028
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: US 09/796,720
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/828,035
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 09/833,081
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 09/843,128
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/957,683
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: US 09/964,252
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 09/964,256
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 10/024,623
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 1262
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (15)..(1136)
US-10-146-733-40

Alignment Scores:
Pred. No.: 2,45e-116 Length: 1262
Score: 1100.00 Matches: 229
Percent Similarity: 67.07% Conservative: 48
Best Local Similarity: 55.45% Mismatches: 86
Query Match: 52.26% Indels: 50
DB: 16 Gaps: 5

US-09-939-483-5 (1-405) x US-10-146-733-40 (1-1262)
Qy 1 GluAsnValArgThrLeuAlaLeuIleValCysThrPheThrTyrLeuLeuValGlyAla 20
Db 24 CAGAACGTGCGGACTCTGCTCCCTCATCTGTCACCTTCACTACCTGCTGTGGCGCC 83
Qy 21 AlaValPheAspAlaLeuGluSerGluProGluMetIleGluArgGlnArgLeuGluLeu 40
Db 84 GCCGTGTTCGACGCCCTCGAGTCGGACCCAGATGCGCGAGGAGGAGAACTCAAAGCC 143
Qy 41 ArgGlnLeuGluLeuArgAlaArgTyrAsnLeuSerGluGlyGlyTyrGluGluLeuGlu 60
Db 144 GAGGAGATCCCGGATCAAGGGGGAATCAACATCAGCAGCAGGAGACTACCGCGCTGGAG 203
Qy 61 ArgValValLeuArgLeuLysProHisLysAlaGlyValGlnTrpArgPheAlaGlySer 80
Db 204 CTGTGTATCTGTCAGTCCGACCCGCGCGGTCTCCAGTGGAAATTCGCGGCTCC 263
```

```
Qy 81 PheTyrPheAlaIleThrValIleThrThrIleGlyTyrGlyHisAlaAlaProSerThr 100
Db 264 TTCTACTTTGGATCATCGGTTCATCCACCATAGTTATGGGCACGCTGCACCTGGGCACC 323
Qy 101 AspGlyGlyLysValPheCysMetPheTyrAlaLeuLeuGlyIleProLeuThrLeuIle 120
Db 324 GATCGGGCAAGGCTTCTGCATGTTCTACGCCGTGCTGGGCATCCCGCTGCACACTGGTC 383
Qy 121 MetPheGlnSerLeuGlyGluArgIleAsnThrPheValArgTyrLeuLeuHisArgAla 140
Db 384 ATGTTTCAGAGCCCTGGGGCAGCGATGAACACCTTCGTGGCGTACCTGCTGAAGCGGATT 443
Qy 141 LysArgGlyLeuGlyMetArgHisAlaGluValSerMetAlaAsnMetValLeuIleGly 160
Db 444 AAGAAGTCTGTGCATGGCGCAACACTGACGTGCTATGGAGAACATGGTGACTGTGGC 503
Qy 161 PheValSerCysIleSerThrLeuCysIleGlyAlaAlaPheSerTyrTyrGluArg 180
Db 504 TTCTTCTCTGCATGGGACGCTGTGCATCGGGCGCGCCTTCTCCAGTGTGAGGAG 563
Qy 181 TrpThrPhePheGlnAlaTyrTyrCysPheIleThrThrIleGlyPheGly 200
Db 564 TGGAGCTTCTTCCAGCGCTACTACTGCTTCATCAGTTGACTACCATTTGGGTTCCGG 623
Qy 201 AspTyrValAlaLeuGlnLysAspGlnAlaLeuGlnThrGlnProGlnTyrValAlaPhe 220
Db 624 GACTACGTGGCCCTGCAGACCAAGGGCGCCTGCAGAAAGCGCTCTACGTGGCCTTT 683
Qy 221 SerPheValTyrIleLeuThrGlyLeuThrValIleGlyAlaPheLeuAsnLeuVal 240
Db 684 AGCTTTATGATATCTTGGTGGGCTGACGGTCACTCGGGCGCTTCTCAACCTGGTGGTC 743
Qy 241 LeuArgPheMetThrMetAsnAlaGluAspGluLysArgAspAlaGluHisArgAlaLeu 260
Db 744 CTCAGGTTCTTGACCATGAACAGAGGATGAGCGCGGATGCTGAAGAGAGGGCATCC 803
Qy 261 LeuThrHisAsnGlyGlnAlaValGlyLeuGlyLeuSerCysLeuSerGlySerLeu 280
Db 804 CTCGCGGAAACCGCAAC-----AGCATGGTTCATTCACATCCCT 842
Qy 281 GlyAspValArgProArgAspProValThrCysAlaAlaAlaGlyValGlyVal 300
Db 843 GAGGAGCGCGCGCGCAGCGGCC----- 866
Qy 301 GlyValGlyGlySerGlyPheArgAsnValTyrAlaGluValLeuHisPheGlnSerMet 320
Db 867 -----AGGTACAGCGGACGCTCCGCGACCTGCAGTCTGTG 902
Qy 321 CysSerCysLeuTrpTyrLysSerArgGluLysLeuGlnTyrSerIleProMetIleIle 340
Db 903 TGCTCTGCACCTGCTACCGCTCGCAGAGC-----TATGGCGCGCGCTCGGTGGCA 953
Qy 341 ProArgAspLeuSerThrSerAspThrCysValGluHisSerHisSer----- 356
Db 954 CCGCAGAACTCTTTCAGCGCGCAAGCTTGCCCCCACTACTTCCACTCATCTCTTACAAG 1013
Qy 357 -----SerProGlyGlyGlyArgTyrSerAspThrProSerHisProCys 372
Db 1014 ATCAGAGAGATCTCACCAGC-----ACA 1037
Qy 373 LeuCysSerGlyThrGlnArgSerAlaIleSerSerValSerThrGlyLeuHisSerLeu 392
Db 1038 TTAAAAACAGCCCTCTCCCATCGCTATTAGCTCCATCTCTCTGGGTTACAGAGTTT 1097
Qy 393 AlaAlaPheArgGlyLeuMetLysArgArgSerSerVal 405
Db 1098 ACCGACCACAGAGGCTGATGAACCGCGGAAGTCCGTT 1136
```

RESULT 13

US-09-798-584-5
; Sequence 5, Application US/09798584
; Patent No. US20020102676A1
; GENERAL INFORMATION:

; APPLICANT: Mu, David
; APPLICANT: Powers, Scott
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: KCNB: A No. US20020102676A1el Potassium Channel Protein
; FILE REFERENCE: 018781-004010US
; CURRENT APPLICATION NUMBER: US/09798, 584
; CURRENT FILING DATE: 2001-03-03
; PRIOR APPLICATION NUMBER: US 60/186,951
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 2312
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: full length cDNA including 5' and 3' UTRs from
; OTHER INFORMATION: breast cancer cell line ZR7530
; NAME/KEY: CDS
; LOCATION: (41)..(1165)
; OTHER INFORMATION: human KCNB (Potassium Channel expressed in Breast)
; US-09-798-584-5

Alignment Scores:

Pred. No.:	6.02e-116	Length:	2312
Score:	1100.00	Matches:	229
Percent Similarity:	67.07%	Conservative:	48
Best Local Similarity:	55.45%	Mismatches:	86
Query Match:	52.26%	Indels:	50
DB:	9	Gaps:	5

US-09-939-483-5 (1-405) x US-09-798-584-5 (1-2312)

```
Qy 1 GluAsnValArgThrLeuAlaLeuIleValCysThrPheThrTyrLeuLeuValGlyAla 20
Db 50 CAGAACGTGGGACTCTGTCCCTCATCGTTCACCTTACCTTACCTGCTGTGGCGGCC 109
Qy 21 AlaValPheAspAlaLeuGluSerGluProGluMetIleGluArgGlnArgLeuLeu 40
Db 110 GCCGTGTTCCACGCCCTCGAGTCGGACGACGATGCGGAGGAGGAGAAACTCAAAGCC 169
Qy 41 ArgGlnLeuGluLeuArgAlaArgTyrAsnLeuSerGluGlyTyrGluGluLeuGlu 60
Db 170 GAGGAGATCCGGATCAAGGGGAAGTACAACATCAGCAGCAGGAGACTACCGGAGCTGGAG 229
Qy 61 ArgValValLeuArgLeuLysProHisLysAlaGlyValGlnTrpArgPheAlaGlySer 80
Db 230 CTGCTGATCTCTGAGTCGGAAACCGCACCGCGCGGCTCCAGTGGAAATTCGCGCGCTCC 289
Qy 81 PheTyrPheAlaIleThrValIleThrThrIleGlyTyrGlyHisAlaAlaProSerThr 100
Db 290 TTCTACTTTGCGATCAGGTTCATCACCATAGTTATGGGCACGCTGCACCTGGCACC 349
Qy 101 AspGlyGlyLysValPheCysMetPheTyrAlaLeuLeuGlyIleProLeuThrLeuIle 120
Db 350 GATCGCGCAAGGCTTCTGCATGTTCTACGCGCTGCTGGGCATCCGCTGCACACTGGTC 409
Qy 121 MetPheGlnSerLeuGlyGluArgIleAsnThrPheValArgTyrLeuLeuHisArgAla 140
Db 410 ATGTTTCAGAGCCCTGGGGCAGCGATGAACACCTTCGTGGCGTACCTGCTGAAGCGGATT 469
Qy 141 LysArgGlyLeuGlyMetArgHisAlaGluValSerMetAlaAsnMetValLeuIleGly 160
Db 470 AAGAAGTGTGTGGATGCGCAACACTGACGTGCTATGGAGAACATGGTGACTGTGGGC 529
Qy 161 PheValSerCysIleSerThrLeuCysIleGlyAlaAlaPheSerTyrTyrGluArg 180
Db 530 TTCTTCTCTGCATGGGACGCTGTGCATCGGGCGCGCCTTCTCCAGTGTGAGGAG 589
Qy 181 TrpThrPhePheGlnAlaTyrTyrCysPheIleThrThrIleGlyPheGly 200
Db 590 TGGAGCTTCTTCCAGCGCTACTACTGCTTCTCATCGCTTGACTACCATTTGGGTTCCGGG 649
```

```
Qy 201 AspTyrValAlaLeuGlnLysAspGlnAlaLeuGlnThrGlnProGlnTyrValAlaPhe 220
Db 650 GACTACGTGGCCCTGCGACCAAGCGGCCCTGAGAGAGAGCGGCTCTACGTGGCCCTTT 709
Qy 221 SerPheValTyrIleLeuThrGlyLeuThrValIleGlyAlaPheLeuAsnLeuValVal 240
Db 710 AGCTTTATGATATCTTGGTGGGCTGACGGTCACTCGGGGCTTCTCAACCTGGTGGTC 769
Qy 241 LeuArgPheMetThrMetAsnAlaGluAspGluLysArgAspAlaGluHisArgAlaLeu 260
Db 770 CTCAGGTTCTTGACCATGACAGTGAAGTGAAGCGGGGATGCTGAAGAGAGGCGCATCC 829
Qy 261 LeuThrHisAsnGlyGlnAlaValIleGlyLeuGlyGlyLeuSerCysLeuSerGlySerLeu 280
Db 830 CTCGCCGGAACCCCAAC-----AGCATGGTCAATTCACATCCCT 868
Qy 281 GlyAspValArgProArgAspProValThrCysAlaAlaAlaGlyGlyValIleGlyVal 300
Db 869 GAGAGCGCGGCCCGCCGCGCC-----AGGTACAAAGCGGAGCTCCCGGACCTGCAGTCTGTG 928
Qy 301 GlyValGlyGlySerGlyPheArgAsnValTyrAlaGluValLeuHisPheGlnSerMet 320
Db 893 -----AGGTACAAAGCGGAGCTCCCGGACCTGCAGTCTGTG 928
Qy 321 CysSerCysLeuTyrTyrLysSerArgGluLysLeuGlnTyrSerIleProMetIleIle 340
Db 929 TGCTCTCGCACTGCTACCGCTCGCAGAC-----TATGCGCGCGCTCGGTGGCA 979
Qy 341 ProArgAspLeuSerThrSerAspThrCysValGluHisSerHisSer-----356
Db 980 CCGCAGAACTCTTCAGCGCCCAAGCTTGCCCCCCTACTTCCACTCCATCTCTTACAAG 1039
Qy 357 -----SerProGlyGlyGlyGlyArgTyrSerAspThrProSerHisProCys 372
Db 1040 ATCGAGGAGATCTCACCAAGC-----ACA 1063
Qy 373 LeuCysSerGlyThrGlnArgSerAlaIleSerSerValSerThrGlyLeuHisSerLeu 392
Db 1064 TTAATAAACACGCTCTTCCCACTCCCTATTAGCTCCCATCTCTCTGGGTTACACAGCTTT 1123
Qy 393 AlaAlaPheArgGlyLeuMetLysArgSerVal 405
Db 1124 ACCGACCACGAGGCTGATGAACCGCGGAAGTCCGTT 1162

RESULT 14
US-09-746-491-56
; Sequence 56, Application US/09746491
; Patent No. US20020137202A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: No. US20020137202A1el Proteins and Nucleic Acids_Encoding Same
; FILE REFERENCE: 15966-621
; CURRENT APPLICATION NUMBER: US/09/746,491
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: USN 60/171,329
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 1286
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-746-491-56

Alignment Scores:
Pred. No.: 1,67e-87 Length: 1286
Score: 850.50 Matches: 199
Percent Similarity: 61.89% Conservative: 43
Best Local Similarity: 50.90% Mismatches: 95
Query Match: 40.40% Indels: 58
DB: 9 Gaps: 7

US-09-939-483-5 (1-405) x US-09-746-491-56 (1-1286)
```

```
Qy 2 AsnValargThrLeuAlaLeuIleValCyeThrPheThrTyrLeuLeuValGlyAlaAla 21
Db 77 AGCGTGGCGCGCGCGCGCTGGTCTGTGTGACCCCTGTGTGTACCTGTGTGGTGGCGCTGCT 136
Qy 22 ValPheAspAlaLeuGluSerGluProGluMetIleGluArgGlnArgLeuGluLeuArg 41
Db 137 GTCTTCACCGCTTCGAGTCCGAGGCGGAAGCGCGCGCGCGAGCTGTGCTGCAGAG 196
Qy 42 GlnLeuGluLeuArgAlaArgTyrAsnLeuSerGluGlyGlyTyrGluGluLeuGluArg 61
Db 197 CGGGCGCTCTCCGGAGGAAGTTCCGCTTCTCGGCCGAGGACTACCGGAGCTGGAGCGC 256
Qy 62 ValValLeuArgLeuLysProHisLysAlaGlyValGlnTrpArgPheAlaGlySerPhe 81
Db 257 CTGGCGCTCCAGGCTGAGCCCAACCGCGCGCGCGCGCAGTGAAGTTTCCCGGCTCCTTC 316
Qy 82 TyrPheAlaIleThrValIleThrThrIleGlyTyrGlyHisAlaAlaProSerThrAsp 101
Db 317 TACTTCGCCATCACCGTCATCATCTACCGGTACGCGCACCGCGCGCGCGGTACGGAC 376
Qy 102 GlyGlyLysValPheCysMetPheTyrAlaLeuLeuGlyIleProLeuThrLeuIleMet 121
Db 377 TCCGGCAAGTCTTCTGCATGTTCTACGCGCTCTTGGGCATCCCGCTGACGCTGGTCACT 436
Qy 122 PheGlnSerLeuGlyGluArgIleAsnThrPheValArgTyrLeuLeuHisArgAlaLys 141
Db 437 TTCAGAGCGCTGGCGAAGCGCTGAAACGCGGTGTGCGCGCTCTCTGTTGGCGGCAAG 496
Qy 142 ArgGlyLeuGlyMetArgHisAlaGluValSerMetAlaAsnMetValLeuIleGlyPhe 161
Db 497 TGTGCTGGCGCTGCGGTGGAGCGTGGGTGTCACGAGAACTGGTGGCGCGGCTG 556
Qy 162 ValSerCysIleSerThrLeuCysIleGlyAlaAlaPheSerTyrTyrGluArgTrp 181
Db 557 CTGGCGTGGCGCGCACCTTGGCCCTCGGGCGCTGCGCTTCTCGCATTCGAGGGGTGG 616
Qy 182 ThrPhePheGlnAlaTyrTyrTyrCysPheIleThrLeuThrThrIleGlyPheGlyAsp 201
Db 617 ACCTTCTTCACGCTACTACTGCTTCACTCCTCATCCCTCACCACCATCGGCTTCGGGAC 676
Qy 202 TyrValAlaLeuGlnLysAspGlnAlaLeuGlnThrGlnProGlnTyrValAlaPheSer 221
Db 677 TTCGTGGCACTGCAGAGCGCGGCGCTGCAGAGGAAGCTCCCTACGTGGCTTCAGC 736
Qy 222 PheValTyrIleLeuThrGlyLeuThrValIleGlyAlaPheLeuAsnLeuValValLeu 241
Db 737 TTCTCTACATCTCTCTGGGGCTCACGGTCAATTGGCGCTTCTCTCAACCTGGTGGTCTG 796
Qy 242 ArgPheMetThrMetAsnAlaGluAspGluLysArgAspAla-----255
Db 797 CGCTTCTCTGTTGCCAGCGCGCAGTGGCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGC 856
Qy 256 -----GluHisArgAlaLeuLeu-----ThrHisAsnGlyGlnAlaVal 268
Db 857 CCCCCCGGGCGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 916
Qy 269 GlyLeuGlyGlyLeuSerCysLeuSerGlySerLeuGlyAspValArgProArgAspPro 288
Db 917 GGCTCCGCTCTGCTCTTCTGCCA-CGTGCACACAGCTGGAGAGGTGCGCGCGCGCAACCT 975
Qy 289 Val-----ThrCysAlaAla-----293
Db 976 GG-GCTTTTTCGCCCCCTCGAGCCCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1034
Qy 294 AlaAlaGlyGly-----ValGlyValGlyValGly 303
Db 1035 GGGCCCGGTGGAGTCCATCTGTACAACCCCAACCCCAACCCCAACCCCAACCCCAACCCCA 1094
Qy 304 GlySerGlyPhe-----ArgAsnVal 310
Db 1095 GGGTCTGGCTTACGTATCAGGGGCAACCTCCCGAGGATGGAAACGAGATGACGGGCTC 1154
```

```
Qy 311 TyxAlaGluValLeuHisPheGlnSerMetCysSerCysLeuTrpTyrIysSerArg--- 329
Db 1155 TAGCGGT-CTTCGACGAGCAAGTTCTCACTACTGTCTGTGGCT-AGTCCCTCCC 1212
Qy 330 -----GluLysLeuGlnTyrSerIleProMet 338
Db 1213 TTTCTTCCAAATAATATTACAGTCACCCCA 1245

RESULT 15
; Sequence 57, Application US/09746491
; Patent No. US20020137202A1
; GENERAL INFORMATION:
; APPLICANT: Burges, Catherine E.
; TITLE OF INVENTION: No. US20020137202A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-621
; CURRENT APPLICATION NUMBER: US/09746,491
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: USN 60/171,329
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57
; LENGTH: 1286
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-746-491-57

Alignment Scores:
Pred. No.: 1,67e-87 Length: 1286
Score: 850.50 Matches: 199
Percent Similarity: 61.89% Conservative: 43
Best Local Similarity: 50.90% Mismatches: 95
Query Match: 40.40% Indels: 58
DB: 7 Gaps: 7

US-09-939-483-5 (1-405) x US-09-746-491-57 (1-1286)
Qy 2 AsnValArgThrLeuAlaLeuIleValCysThrPheThrTyrLeuLeuValGlyAlaAla 21
Db 77 AGCGTGGCGCGCGCGCGCGTGGTCTGTGCACCTGTGTACCTGTGTGGTGGCGGTGCT 136
Qy 22 ValPheAspAlaLeuGluSerGluProGluMetIleGluArgGlnArgLeuGluLeuArg 41
Db 137 GTCTTCACGCGCTCGAGTCCGAGGCGGAAGCGCGCGCGCGCGCTGCTGCTCCAGAAG 196
Qy 42 GlnLeuGluLeuArgAlaArgTyrAsnLeuSerGluGlyTyrGlnGluLeuGluArg 61
Db 197 CGGGCGCGCTCTCCGGAGGAAGTTGGCTTCTCGGCGGAGGACTACCGCGAGCGC 256
Qy 62 ValValLeuArgLeuLysProHisLysAlaGlyValGlnTrpArgPheAlaGlySerPhe 81
Db 257 CTGGCGCTCCAGGCTGAGCCCGCCCGCGCGCGCGCGCGCGCGCGCGCTCTCTTC 316
Qy 82 TyrPheAlaIleThrValIleThrThrIleGlyTyrGlyHisAlaAlaProSerThrAsp 101
Db 317 TACTTCGCCATCACCCTCATCCTACCATCGGTACGGCCACCGCGCGCGCGGTACGGAC 376
Qy 102 GlyGlyLysValPheCysMetPheTyrAlaLeuLeuGlyIleProLeuThrLeuIleMet 121
Db 377 TCCGGCAAGGTCTTCTGTCATGTTCACGCGCTCTCGGGCATCCCGCTGACGCTGGTCACT 436
Qy 122 PheGlnSerLeuGlyGluArgIleAsnThrPheValArgTyrLeuLeuHisArgAlaLys 141
Db 437 TTCAGAGCTGGCGCAACCGCTGACCGCGGTGTGGCGCGCTCTCTCTTTGGCGGCAAG 496
Qy 142 ArgGlyLeuGlyMetArgHisAlaGluValSerMetAlaAsnMetValLeuIleGlyPhe 161
Db 497 TGCTGCTGGCGCTGCGGTGGACGTGCTGTCCACGGAGAACCTGGTGGTGGCGGCGCTG 556
Qy 162 ValSerCysIleSerThrLeuCysIleGlyAlaAlaPheSerTyrTyrGluArgTrp 181
Db 557 CTGGCGGTGCCGCCACCCCTGGGCGCGCTGCGCTTCTCGCACTTCGAGGCGGTGG 616
```

```
Qy 182 ThrPhePheGlnAlaTyrTyrCysPheIleThrLeuThrThrIleGlyPheGlyAsp 201
Db 617 ACCTTTTTCACCGCTTACTACTCTCTCATCACCCTCACCACCATCGCTTCGGCGAC 676
Qy 202 TyrValAlaLeuGlnLysAspGlnAlaLeuGlnThrGlnProGlnTyrValAlaPheSer 221
Db 677 TTCGTGGCACTGCAGAGCGCGAGCGCTGCAGAGGAAGTCCCTTACGTGGCTTCAGC 736
Qy 222 PheValTyrIleLeuThrGlyLeuThrValIleGlyAlaPheLeuAsnLeuValValLeu 241
Db 737 TTCCTCTACATCTCTCGGGCTCAGGTCAITGGCGCTTCTCAACCTGGTGGTCTG 796
Qy 242 ArgPheMetThrMetAsnAlaGluAspGluLysArgAspAla----- 255
Db 797 CGTTTCTGTGTCGACGCGCGGCTGCGCGCGGCTGCGCGCGCGCGCGCGCGCGCGC 856
Qy 256 -----GluHisArgAlaLeuLeu-----ThrHisAsnGlyGlnAlaVal 268
Db 857 CCGCGGGGGCGCGCGAGAGCGTGGCTCTGGCTGCGCGCGCGCGCGCGCGCGCTCG 916
Qy 269 GlyLeuGlyGlyLeuSerCysLeuSerGlySerLeuGlyAspValArgProArgAspPro 288
Db 917 GGCTCGCGCTCTGTCTTCTGCCA-CGTGCACAAGCTGGAGAGTGGCGCGCGCAACCT 975
Qy 289 Val-----ThrCysAlaAla----- 293
Db 976 GG-GCTTTTCGCGCGCGCTGAGCGCGGGGTCTGTGCGGGCGAGGCTCCAGGCGCTG 1034
Qy 294 AlaAlaGlyGly-----ValGlyValGlyValGly 303
Db 1035 GGGCGCGGTGGAAGTCCATCTGACACCCACCCAGCGCGAGGTCTGAAATCTGGAATGGA 1094
Qy 304 GlySerGlyPhe-----ArgAsnVal 310
Db 1095 GGCTCTGGCTTTCAGCTATCAGGCGACCTCCCGAGGGATTTGGAACGAGATGACGGCCTC 1154
Qy 311 TyrAlaGluValLeuHisPheGlnSerMetCysSerCysLeuTrpTyrIysSerArg--- 329
Db 1155 TAGCGGT-CTTCGACGAGCAAGTTCTCACTACTGTCTGTGGCT-AGTCCCTCCC 1212
Qy 330 -----GluLysLeuGlnTyrSerIleProMet 338
Db 1213 TTTCTTCCAAATAATATTACAGTCACCCCA 1245
```

Search completed: September 16, 2005, 08:00:39
Job time : 2225 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2005, 22:47:23 ; Search time 40 Seconds
(without alignments)
974.195 Million cell updates/sec

Title: US-09-939-483-5
Perfect score: 2105
Sequence: 1 ENVRTLALIVCTFTYLLVGA.....STGLHSLAARGLMKRRSSV 405

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	836.5	39.7	330	JC7703	TASK-5 protein - h
2	800	329	2	T43509	probable potassium
3	788.5	37.5	336	T32347	outward rectifier
4	611	29.0	334	T19860	hypothetical prote
5	611	29.0	364	T43361	probable potassium
6	334.5	15.9	336	S65566	inward rectifier p
7	305.5	14.5	513	T28933	hypothetical prote
8	303.5	14.4	393	T25392	hypothetical prote
9	289	13.7	524	T32907	hypothetical prote
10	282	13.4	1539	T30037	hypothetical prote
11	276.5	13.1	1001	T13807	potassium channel
12	273.5	13.0	1910	H88124	protein t12c9.3 [i
13	269.5	12.8	383	T23182	hypothetical prote
14	266	12.6	443	T21598	hypothetical prote
15	262	12.4	427	T27681	hypothetical prote
16	261.5	12.4	335	S44635	f2b27.7 protein -
17	255	12.1	452	T21118	hypothetical prote
18	255	12.1	569	T43531	probable potassium
19	251.5	11.9	392	T45032	hypothetical prote
20	248	11.8	544	T43364	potassium channel
21	248	11.8	576	T43363	potassium channel
22	247	11.7	528	T21834	hypothetical prote
23	246	11.7	444	T26229	hypothetical prote
24	244	11.6	475	T27725	hypothetical prote
25	241.5	11.5	522	T24265	hypothetical prote
26	241	11.4	381	T43393	potassium channel
27	237.5	11.3	325	T15584	hypothetical prote
28	237.5	11.3	461	T43394	potassium channel
29	236	11.2	769	T27550	hypothetical prote

30	235.5	11.2	600	2	T24626	hypothetical prote
31	227.5	10.8	485	2	T24201	hypothetical prote
32	223.5	10.6	1136	2	T26953	hypothetical prote
33	217	10.3	643	2	T26616	hypothetical prote
34	216	10.3	539	2	T23700	hypothetical prote
35	216	10.3	586	2	T21683	hypothetical prote
36	214.5	10.2	484	2	T43529	probable potassium
37	214.5	10.2	519	2	T16629	hypothetical prote
38	214.5	10.2	551	2	T16426	hypothetical prote
39	214.5	10.2	555	2	T43357	potassium channel
40	213.5	10.1	350	2	T15178	hypothetical prote
41	210.5	10.0	504	2	T22269	hypothetical prote
42	208.5	9.9	660	2	T21551	hypothetical prote
43	204.5	9.7	700	2	T27364	hypothetical prote
44	195	9.3	383	2	T23746	hypothetical prote
45	187.5	8.9	631	2	T26232	hypothetical prote

ALIGNMENTS

RESULT 1
JC7703
TASK-5 protein - human
C:Species: Homo sapiens (man)
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C:Accession: JC7703
R:Kim, D.; Gnatenco, C.
Biochem. Biophys. Res. Commun. 284, 923-930, 2001
A:Title: TASK-5, a new member of the tandem-pore K+ channel family.
A:Reference number: JC7703; MUID:21303050; PMID:11409881
A:Accession: JC7703
A:Molecule type: DNA
A:Residues: 1-330 <KIM>
A:Cross-references: GB:ML118522
C:Comment: This protein, a new member of the tandem-pore K+ channel family with four tra
hormone secretion, but does not produce a functional plasma membrane K+ current by itsel

C:Genetics:
A:Gene: task-5
A:Map position: 20q12
C:Keywords: transmembrane protein
F:7-30/Domain: transmembrane segment #status predicted <TMS1>
F:107-128/Domain: transmembrane segment #status predicted <TMS2>
F:129-155/Region: hydrophobic cytoplasmic linker #status predicted
F:156-180/Domain: transmembrane segment #status predicted <TMS3>
F:220-240/Domain: transmembrane segment #status predicted <TMS4>

Query Match		39.7%;	Score	836.5;	DB 2;	Length	330;
Best Local Similarity		54.6%;	Pred. No.	1.1e-65;			
Matches		179;	Conservative	35;	Mismatches	83;	Indels 31; Gaps 3;
Qy	2	NVRTLALIVCTFTYLLVGA	AVFDAL	SEPEMERQRL	LELRQLELRARVNL	SEGVEELER	61
Db	5	SVRAAGLVICTLCVLLVGA	AVFDAL	SESGRQLLVQK	GRLLRRKFGFSA	EDYRELER	64
Qy	62	VVLRLPKHAGVQWR	FAGSFY	FAITVTIT	TIGYGHAA	STDGGKVF	FCMFYALLGLPTLIM 121
Db	65	LALQAEPRHAGRWK	FPGSFY	FAITVTIT	TIGYGHAA	PTDGSQKVF	FCMFYALLGLPTLTV 124
Qy	122	FQSGERINTFVRL	LHRAKGLG	MRHAESV	MANMVLIG	FVSCISTLC	IGAAFSYVERW 181
Db	125	FQSGERLNAVVR	LLLAAC	CCGLRWTC	STENLVAG	LACCAATL	ALGAVAFSHFEGW 184
Qy	182	TFQAYYCYFTL	TITIGFDY	VALQKDQ	ALQTOQ	PQYVAFS	FVYILGTIGTIGAFNLVVL 241
Db	185	TFFHAYYCYFTL	TITIGFDV	ALQS	GEALQK	LPYVAFS	FLYLLGLTIGTIGAFNLVVL 244
Qy	242	RFMTMNADEK	RDA-----	EHRL	LTHNQAV	GLGGLS-----	CLSGSL 280
Db	245	RFLVASADWP	EAAART	TPSPPG	APESRGL	WLPRRPAR	SVGSASFCHVHKLERCARDNL 304
Qy	281	GDVPRDVT	CAAAAG	GVGVG	GVGSGPR	308	

Db 305 GFSPSPSP-----GVRGGQAPR 322

RESULT 2

T43509

probable potassium channel chain n2P38 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004

C;Accession: T43509

R;Wang, Z.W.; Salkoff, L.

submitted to the EMBL Data Library, August 1998

A;Description: Potassium channels in C. elegans.

A;Reference number: Z22450

A;Accession: T43509

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-329 <MAN>

A;Cross-references: UNIPROT:O17185; EMBL:AF083652; PIDN:AAC32863.1

Query Match 38.0%; Score 800; DB 2; Length 329;

Best Local Similarity 47.8%; Pred. No. 1.8e-62;

Matches 175; Conservative 51; Mismatches 82; Indels 58; Gaps 10;

Qy 1 ENVRTLALIVCTFTYLLVGAADFDALESEPEMIRORLELRQLELRARYNLSEGGYEELE 60

Db 4 QNIRTLSLIVCTLTLYLLVGAADFDALESEPEMIRORLELRQLELRARYNLSEGGYEELE 63

Qy 61 RVVLRRLKPHKAGVQWRFGAGSFYFAITVITTYGYGHAAPSTDGKGVCFCMFYALLGIPLTLI 120

Db 64 ATIVKSVPHKAGYQWKFSGAFYFATVITTYGYGHSPTMDAGKFCMLYALAGIPLGLI 123

Qy 121 MFQSLGERINTFVRYLLHRAKRGIMRHAESVMANMVLIGFVSCISTLCI--GAAPFSYY 178

Db 124 MFQSIGERMNTFAAKLRFIRRAAG-KQPIVTSSDLII--FCTGWGGLLIFFGAFMFSY 180

Qy 179 ERWTFQAYYCFITLTITGFDYVALQKQALQTOQYVAFSPYVILGTIGVAPLNL 238

Db 181 ENWTFYDAVYCFVTLTTITGFDYVALQKQSLQTOPEYVFFSLVFLTGLTIVISAANL 240

Qy 239 VLRFTMTNAEDKRDHRAHLLTHNGQAVGLGSLGCLSGLDGVRPRDPVTCAAAAGV 298

Db 241 LVLRFLTNWTEDEKRD--EQEAILAAQ--LVRVGDPTA-DDDFGRLPLSDNVSL 292

Qy 299 GVGVGSGFRNVYAEVLHFQSMCSCLWYKREKLQYISIPMIIPRDLSTSDTCVEH---SH 355

Db 293 -----CSC-----YQLP-----DEKLRRHRKH 310

Qy 356 SSPGGG 361

Db 311 TEPRGG 316

RESULT 3

T32347

outward rectifier potassium channel homolog twk-23 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C;Accession: T32347

R;Murray, J.; Wohlmann, P.; O'Neal, D.

submitted to the EMBL Data Library, September 1997

A;Description: The sequence of C. elegans cosmid F34D6.

A;Reference number: Z21153

A;Accession: T32347

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-336 <MUR>

A;Cross-references: UNIPROT:O17185; EMBL:AF025454; PIDN:AAC71151.1; GSPDB:GN000020; CESP:

A;Experimental source: strain Bristol N2; clone F34D6

C;Genetics:

A;Gene: twk-23; CESP:F34D6.3

A;Map position: 2

A;Introns: 44/3; 102/1; 136/1; 180/1; 207/1; 265/2; 296/3

Query Match 29.0%; Score 611; DB 2; Length 334;

Best Local Similarity 47.7%; Pred. No. 7.1e-46;

Matches 123; Conservative 45; Mismatches 78; Indels 12; Gaps 3;

Qy 1 ENVRTLALIVCTFTYLLVGAADFDALESEPEMIRORLELRQLELRARYNLSEGGYEELE 60

Db 7 KSARALLILSTFTYLLFGAMVDFKLESEKDTWVRDEIERITDLRKHKYNFSDRLHLFE 66

Qy 61 RVVLRRLKPHKAGVQWRFGAGSFYFAITVITTYGYGHAAPSTDGKGVCFCMFYALLGIPLTLI 120

Db 67 AIAIKSIPQAGYQWQFAGAFYFATVITTYGYGHSAPSTNAGKLCMIFALGVPMGLI 126

Qy 121 MFQSLGERINTFVRYLLHRAKRGIMRHAESVMANMVL-----IGFVSCISTLCIGA 172

Db 127 MFQSIGERMNTFIAYSLHFRDSLHQGGFTCLQEVPTPTLLMVLSTIGFWMVVS---GT 182

Qy 173 AAPFSYERWTFQAYYCFITLTITGFDYVALQKQALQTOQYVAFSPYVILGTITVI 232

Db 183 YMFHTTKRSIFDAYYFCMNTFTTIGFDGLVPLQVQNALQDQDPLYVVFATIMFILGLAVF 242

Query Match 37.5%; Score 788.5; DB 2; Length 336;

Best Local Similarity 47.7%; Pred. No. 1.9e-61;

Matches 178; Conservative 49; Mismatches 81; Indels 65; Gaps 12;

Qy 1 ENVRTLALIVCTFTYLLVGAADFDALESEPEMIRORLELRQLE-----ELARAYNLSE 53

Db 4 QNIRTLSLIVCTLTLYLLVGAADFDALESEPEMIRORLELRQLELRARYNLSEKKTKYNSN 63

Qy 54 GGYEELERVVRLKPHKAGVQWRFGAGSFYFAITVITTYGYGHAAPSTDGKGVCFCMFYALL 113

Db 64 ADVEILEATIVKSVPHKAGYQWKFSGAFYFATVITTYGYGHSPTMDAGKFCMLYALA 123

Qy 114 GIPLTLIMFQSLGERINTFVRYLLHRAKRGIMRHAESVMANMVLIGFVSCISTLCI--G 171

Db 124 GIPLGLIMFQSIGERMNTFAAKLRFIRRAAG-KQPIVTSSDLII--FCTGWGGLLIFFG 180

Qy 172 AAPFSYERWTFQAYYCFITLTITGFDYVALQKQALQTOQYVAFSPYVILGTITVI 231

Db 181 AFNFSSYENWTFYDAVYCFVTLTTITGFDYVALQKQSLQTOPEYVFFSLVFLTGLTV 240

Qy 232 IGAFPLNLVLRFTMTNAEDKRDHRAHLLTHNGQAVGLGSLGCLSGLDGVRPRDPVTC 291

Db 241 ISAMNLLVLRFTMTNTEDEKRD--EQEAILAAQ--LVRVGDPTA-DDDFGRLPLSDNVSL 297

Qy 292 AAAAGVGVGSGFRNVYAEVLHFQSMCSCLWYKREKLQYISIPMIIPRDLSTSDTCV 351

Db 298 AS-----CSC-----YQLP-----DEKL 310

Qy 352 EH---SHSPGGG 361

Db 311 RHRHRKHTEPHGG 323

RESULT 4

T19860

hypothetical protein C40C9.1 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C;Accession: T19860

R;Hembry, C.

submitted to the EMBL Data Library, March 1996

A;Reference number: Z19188

A;Accession: T19860

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-334 <WIL>

A;Cross-references: EMBL:Z70266; PIDN:CAA94204.1; GSPDB:GN000028; CESP:C40C9.1

A;Experimental source: clone C40C9

C;Genetics:

A;Gene: CESP:C40C9.1

A;Map position: X

A;Introns: 34/1; 60/2; 98/1; 145/3; 160/3; 181/1; 204/1; 252/2; 279/2; 306/3

QY 233 GAFLNLVLRFTMNAED 250
DB 243 SACVNLVLGFMASNADE 260

RESULT 5
T43361
probable potassium channel chain n2p20 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
R:Wang, Z.W.; Salkoff, L.
submitted to the EMBL Data Library, August 1998
A:Description: Potassium channels in C. elegans.
A:Reference number: Z22450
A:Accession: T43361
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-364 <MAN>
A:Cross-references: UNIPROT:O76790; EMBL:AF083646; PIDN:AAC32857.1

Query Match 29.0%; Score 611; DB 2; Length 364;
Best Local Similarity 47.7%; Pred. No. 7.9e-46;
Matches 123; Conservative 45; Mismatches 78; Indels 12; Gaps 3;

QY 1 ENVRTALIVCTFTYLLVGAAVFDALSEPEMERQRLQLELRARYNLSEGGYELE 60
DB 7 KSARALLILSTFTYLLGAMVFDKLESEKDTWVRDEITERIDRLKHKNFSERDLHLFE 66
QY 61 RVVLRLEKPKAGVQWRPAGSFYFALTITTTIGYGHAAAPSTGGKVFQMFYALIGPLTLI 120
DB 67 AIAIKSIFQQAGYQWQFAGFFATVTTTGVGHSAPSTNAGKLFQMFALFGVPMGLI 126
QY 121 MFQSLGERINTFVRYLLHRAKRGKLMRH-----AEVSMANMVL-----IGFVSCISTLCIGA 172
DB 127 MFQSLGERVNTFIAYLSLHKRDSLHQQGTCLQEVTPTHLMVSLITIGFMIVS-----GT 182
QY 173 AAFSYERWTFFQAYYYCFITLTITIGDGYVALQKQALQTPQVAFSVFVILTGLTVI 232
DB 183 YMFHTIEKWSIFDAYFYFCMITFTSTIGDGLVPLQOVNALQDQVYFATIMFILIGLAVF 242
QY 233 GAFLNLVLRFTMNAED 250
DB 243 SACVNLVLGFMASNADE 260

RESULT 6
S65566
inward rectifier potassium channel TWIK-1 - human
C:Species: Homo sapiens (man)
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S65566
R:Lesage, F.; Guillemare, E.; Fink, M.; Duprat, F.; Lazdunski, M.; Romey, G.; Barhanin, EMO J. 15, 1004-1011, 1996
A:Title: TWIK-1, a ubiquitous human weakly inward rectifying K(+) channel with a novel a
A:Reference number: S65566; MUID:96183184; PMID:8605869
A:Accession: S65566
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-336 <LES>
A:Cross-references: UNIPROT:O00180; EMBL:U33632; NID:g1086490; PIDN:AAB01688.1; PID:g108

Query Match 15.9%; Score 334.5; DB 2; Length 336;
Best Local Similarity 33.7%; Pred. No. 1.4e-21;
Matches 99; Conservative 47; Mismatches 109; Indels 39; Gaps 11;

QY 8 LIVCTFTYLLVGAAVFDALSEPEMERQRLQLE---LRARYNLSEGGYEELERVVL 64
DB 26 LVLGYYLLLVFGAVVFSVELPYEDLLRQ--ELRKLKRFLSEHSECLSEQLQFLGRVL 83
QY 65 RLKPKHAGV-----QWRPAGSFYFALTITTTIGYGHAAAPSTGGKVFQMFYALIGIP 116
DB 84 EASNYGVSVLSNASGNWWDFTSALFVSTLTGTGHTVPLSDGGKAFCTIIYSVIGIP 143

QY 117 LTLIMFOSLGERINTFV--RYLLHRAKRGKLMRHAEVSMANMVLIGFVSCISTLCIGAA 174
DB 144 FTLLFLTAVQRIITVHVTRRVLVYFHIR-WGFSKQVVAIVHVLVGLFVTVSCFFPIPAV 202
QY 175 FSYVE-RWTRFQAYYYCFITLTITIGDGYVA---LQKQALQTPQVAFSVFVILTG- 228
DB 203 FSVLEDDWNFLSFYFCFISLTIGLDYVPGEGYNQKRFEL-----YKIGITCYLLGL 257
QY 229 ---LTVIGAFNLVVL-RFTMNAEDKRDAAHRLALTHN-----GQAVGL 270
DB 258 IAMLVVLTEFCELHELKFKRMFVVKDKDQVHIIHEDQLSFSSITDQAAGM 311

RESULT 7
T28933
hypothetical protein C52B9.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C:Accession: T28933
R:Nelson, J.
submitted to the EMBL Data Library, July 1996
A:Description: The sequence of C. elegans cosmid C52B9.
A:Reference number: Z20545
A:Accession: T28933
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-513 <NBL>
A:Cross-references: EMBL:U64598; PIDN:AAC47976.1; GSPDB:GNO0028; CESP:C52B9.6
A:Experimental source: strain Bristol N2; clone C52B9
C:Genetics:
A:Gene: CESP:C52B9.6
A:Map position: X
A:Introns: 12/3; 54/3; 90/3; 158/1; 173/1; 227/3; 299/3; 346/2; 405/1; 452/3

Query Match 14.5%; Score 305.5; DB 2; Length 513;
Best Local Similarity 25.5%; Pred. No. 7.9e-19;
Matches 94; Conservative 56; Mismatches 104; Indels 115; Gaps 12;

QY 6 LALIVCTFTYLLVGAAVFDALSEPEMERQRLQLELRARYNLSEGGYEELERVVL 65
DB 63 VGLVILLVFLVLIAGAFVLEAPKELESD---NRISREAFNAIQEYFEQLVKNMFQ 118
QY 66 L-----KPHKAGVQWRPAGSFYFALTITIT-----GYGHAA 97
DB 119 AYRNQFITAKHLNKTREDEVLTWTFPNSMFEAATVITTVQKNRSGNRVVFSGYGNLV 178
QY 98 PSTDGGKVFQMFYALIGPLTLIMFQSLGERINTFVRYLLHRAKRG----- 143
DB 179 PITVTVGRVACIIIFALLGIPLLLVTIADIGKPLSEFLSY-LYRSYRGFKRKLRRSKKITS 237
QY 144 -----LGMRHA-----EVSMMANMVLIGFVSCISTL 168
DB 238 QYRSQSOSRSSVNGSSKAGSMNLHIDSDSEDSAGDELRIIPVFMVLLVLLAYTA----- 292
QY 169 CIGAAAFSYERWTFFQAYYYCFITLTITIGDGYVALQKQALQTPQVAFSVFVILTG 228
DB 293 -IGGFLFQSWHELEYEAFYFCFITMATVGFQDIV-----PNEQVYVFFTMAYIIFG 343
QY 229 LTVIGAFNLV-----VLRPMTWNADEK-----RDAEHRALLTHNGQAVGLGGLSC 275
DB 344 LSLATMCIIDLAGTYIRKIHYLGTMKMDAKGAVMTGLQAGEH--LLKHTGIEV-----IKT 397
QY 276 LSGSLGQVR 284
DB 398 AGGKLQVR 406

RESULT 8
T25392
hypothetical protein T28A8.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

QY 289 VTCARAAAGGVGVGSGSF-----RNVYAEVL-HFQSMCS 322
Db 418 NAASAMWAGF---QGRAXPLMLPLISKNEGAKVMDFKQDCS 455

RESULT 11
T13807
potassium channel protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C:Accession: T13807
R:Goldstein, S.A.; Price, L.A.; Rosenthal, D.N.; Pausch, M.H.
Proc. Natl. Acad. Sci. U.S.A. 93, 13256-13261, 1996
A:Title: ORK1, a potassium-selective leak channel with two pore domains cloned from Dros
A:Reference number: Z17770; MUID:97075152; PMID:8917578
A:Accession: T13807
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1001 <COL>
A:CROSS-references: UNIPROT:Q94526; EMBL:U55321; NID:g3808067; PID:g3808068; PIDN:AAC692
C:Genetics:
A:Gene: ORK1
A:CROSS-references: FlyBase:FBgn0017561
A:Map position: 1

Query Match 13.1%; Score 276.5; DB 2; Length 1001;
Best Local Similarity 26.9%; Pred. No. 6.2e-16;
Matches 73; Conservative 60; Mismatches 113; Indels 25; Gaps 8;

QY 4 RTALIVCTFTYLLVGAADFDALESEPEMERQRLLEQLRLARYNLSEGG-----Y 56
Db 5 RWLLILFYISYLMFGAIIYTHIEGSEKISRAEQKQAQAIN-BYLLEELGDKNNTTQD 63

QY 57 BEELERV-----VLRKP--HKAGVQWRFAGSFYFAITVITIGYGHAAAPSTDGKVF 108
Db 64 EILQRISYCDKPVLTPTDYDDPTWTFYHAFPAFTVCSTVGYNISPTTFAGMIMI 123

QY 109 FYALLIGPLTIMFOSLGERIN-----TFVRYLLHRAKRGKGMRAEVSMMANVLIGFVS 163
Db 124 AYSVIGIPVNGILFAGLGEYFRTPEATYRKYKYNSTDMHYVPPQLGLITTVVIALIP 183

QY 164 CIST-LCIGAAAFSYVERWTFFQAYYCFITLTIGFGDYV-ALQKQALQTPQYVAFS 221
Db 184 GIAPFLPLPSWVTFYFENWPSISISYIVTITIGFDYVPTFGANQPKFGWFFVYQ 243

QY 222 FVYILTGLTVIGAFNLVLRFTMTNADEK 252
Db 244 IFVIVWFIFSLGYL--VMIMTFITRGLQSKK 272

RESULT 12
H88124
protein T12C9.3 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C:Accession: H88124
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/projects/C_ele
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: H88124
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1910 <STO>
A:CROSS-references: GB:chr_II; PIDN:AC71141.1; PID:gl086770; GSPDB:GN000020; CESP:T12C9.3
A:Note: proline-rich
C:Genetics:
A:Gene: T12C9.3
A:Map position: 2

Query Match 13.0%; Score 273.5; DB 2; Length 1910;

Best Local Similarity 23.0%; Pred. No. 2.5e-15;
Matches 79; Conservative 53; Mismatches 104; Indels 107; Gaps 8;

QY 1 ENVRTLA-----LIVCTFTYLLVGAADFDALES--EPEMIERQRLLEQLRLARY- 49
Db 189 QNIRKYAKLALPHIVLVVCVCIYATIGAWIFYLTSPNEDRLKETGRTKTAIEMRSNLIYK 248

QY 50 ---NLSEGGYEELERVVL----- 64
Db 249 INNKEVWKEDIEKELMLYSEKLYKAFKEQVRYVSDVRTIGFEGRSYBEADETGDS 308

QY 65 RLKPKHAG-----VQWRFAGSFYFAITVITIGYGHAAAPSTDGKVF 115
Db 309 RKRHRHGNKKGDRGSEKMTTSSALFPAATMATIGYGNIVPVTPGLRLACVLFAFGA 368

QY 116 PTLIMFQSLGERINTFVRYLLHRAKRG----- 143
Db 369 PIAIITIGDLGKFLSECTIMLYKHMKGSAARLSAWEKFRGLEDSDLESASKNQDSS 428

QY 144 -LGRHRAEVSMMANM-VLIGFVSCITLCIGAAAFSYVERWTFFQAYYCFITLTIGFGD 201
Db 429 ILDMDEIDKSEVPVLMVFTIILYIAFGGILFSEILEDWSYMDAFYYSFISLTIGFGD 488

QY 202 YVALQKQALQTPQYVAFSFPVYILTGLTVIGAFNLVLRFM 244
Db 489 IVPENHD-----YIAIMLYIGVLSVVTMCDLAGIOYI 523

RESULT 13
T23182
hypothetical protein K01D12.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T23182
R:Dobson, R.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19703
A:Accession: T23182
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-383 <WIL>
A:CROSS-references: UNIPROT:Q21094; EMBL:Z75543; PIDN:CAA99871.1; GSPDB:GN000023; CESP:K0
A:Experimental source: clone K01D12
C:Genetics:
A:Gene: CESP:K01D12.4
A:Map position: 5
A:Introns: 28/3; 76/3; 184/2; 217/2; 270/2; 295/2

Query Match 12.8%; Score 269.5; DB 2; Length 383;
Best Local Similarity 25.9%; Pred. No. 8.1e-16;
Matches 89; Conservative 57; Mismatches 137; Indels 61; Gaps 9;

QY 1 ENVRTLALIVCTFTYLLVGAADFDALESEPEMIERQRLLEQLRLARY----NLSEGGY 56
Db 40 ENARFVLICILIVLAFGAILFHWLEWENEVDRIADNRMADYQKYCKHKLNECDF 99

QY 57 BEELERVLRKPKHAGV-----QWRFAGSFYFAITVITIGYGHAAAPSTDGKVF 111
Db 100 EEMVRFI--SDGATSGLLNSRSRFDHLGSLFFSATVISTIGFGTSTPRTHLGRFTIIVYG 157

QY 112 LLGLPLTLIMFQSLGERINTFVRYLL-----HRAKR----- 142
Db 158 VVGTCVLPFLPLRLVLTGMSYILRSRLRKRIRYRLKESGNKPVTLNLLNEDFNES 217

QY 143 --GLGMRHAEVSMMANVLIGFVSCITLCIGAAAFSYVERWTFFQAYYCFITLTIGFG 200
Db 218 SCGGHMDNWRPSYKVFIFLPSMCLVITASAGIYSVVENWNYIDSLYFCFISFATIGFG 277

QY 201 DYVALQKQALQTPQY-----VAFSFVYILTGLT--VIGAFNLVLRFMFTMNAE 249
Db 278 DYVSNQDVTWMSPDLYRFVNFVNFCLLTGACFFYCLNSVSSIVVRQLLNMMIKK-MDVKVE 336

QY 250 D-----EKRDARHALLTHNGQAVGLGLGSLGSLGSDVRPR 286

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 16, 2005, 06:00:08 ; Search time 4202 Seconds
(without alignments)
3668.736 Million cell updates/sec

Title: US-09-939-483-5
Perfect score: 2105
Sequence: 1 ENVRTALIVCTYLLVGA.....STGLHSLAARGLMKRRSSV 405

Scoring table: BLOSUM62 Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DBV=xlh
-O=/cgn2_1/USPTO.spool/US0939483/runat_15092005_111400_9726/app_query.fasta_1.583
-DB=EST -QPM=fastap -SUFFIX=ret -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOTALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US0939483 @CGN 1.1 4352 @runat_15092005_111400_9726 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: EST:*

1: gb_est1:.*
2: gb_est2:.*
3: gb_hic:.*
4: gb_est3:.*
5: gb_est4:.*
6: gb_est5:.*
7: gb_est6:.*
8: gb_gsal:.*
9: gb_gss2:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1631.5	77.5	947	9 AY411659	AY411659 Mus muscu
2	1500.5	71.3	1043	3 BC032047	BC032047 Mus muscu
3	1372	65.2	902	3 AY411657	AY411657 Homo sapi
4	1287	61.1	1045	5 BX359243	BX359243 BX359243
5	1279	60.8	874	9 AY411658	AY411658 Pan trogl
6	1246	59.2	995	4 BI412471	BI412471 602985964
7	1230	58.4	789	7 CK602460	CK602460 AGENCOURT
8	1182.5	56.2	881	4 BG750477	BG750477 602709342
9	1153	54.8	1002	1 AL530478	AL530478 AL530478

ALIGNMENTS

LOCUS	AY411659	Mus musculus KNC3 gene, genomic survey sequence.	947 bp	DNA	linear	GSS 16-DEC-2003
DEFINITION	AY411659	Mus musculus KNC3 gene, genomic survey sequence.				
ACCESSION	AY411659	AY411659.1 GI:39767627				
VERSION		GSS				
KEYWORDS		Mus musculus (house mouse)				
SOURCE		Mus musculus				
ORGANISM		Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE		1 (bases 1 to 947)				
AUTHORS		Todd, M.A., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.				
TITLE		Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL		Science 302 (5652), 1960-1963 (2003)				
PUBMED		14671302				
REFERENCE		2 (bases 1 to 947)				
AUTHORS		Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.				
TITLE		Direct Submission				
JOURNAL		Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT		This sequence was made by sequencing genomic exons and ordering them based on alignment.				
FEATURES		Location/Qualifiers				
source		1. .947				

10	1136	54.0	677	1	AI605559	AI605559 ma07h04.y
11	1098.5	52.2	725	5	BX922107	BX922107 BX922107
12	1069.5	50.8	630	2	BF467278	BF467278 UI-M-CG0P
13	1055.5	50.1	665	8	BZ116659	BZ116659 CH230-365
14	1035	49.2	892	5	BX745213	BX745213 BX745213
15	1027.5	48.8	610	2	BF462825	BF462825 UI-M-CG0P
16	1013	48.1	847	6	CD360817	CD360817 AGENCOURT
17	976.5	46.4	574	7	CK345752	CK345752 L0516A06-
18	961	45.7	575	4	BM052871	BM052871 1667406.y
19	953.5	45.3	636	1	AI327069	AI327069 mE89407.x
20	951	45.2	637	5	BU072252	BU072252 im44c06.x
21	946.5	45.0	564	2	BF288999	BF288999 EST453590
22	927	44.0	549	2	BF466470	BF466470 UI-M-CG0P
23	916	43.5	847	7	CK599195	CK599195 AGENCOURT
24	915	43.5	550	7	CK903866	CK903866 1667406.y
25	909	43.2	1020	9	CNS031QR	AL223884 Tetradon
26	907.5	43.1	555	1	AI407650	AI407650 EST235940
27	906	43.0	542	2	AW141881	AW141881 EST291996
28	878	41.7	622	6	CA950044	CA950044 1-86808.y
29	877	41.7	579	2	BF434972	BF434972 7P04406.x
30	875.5	41.6	520	2	BF463979	BF463979 UI-M-CG0P
31	861	40.9	674	2	BE378534	BE378534 601236558
32	858	40.8	631	7	CK778467	CK778467 965628 MA
33	849	40.3	601	6	CB067409	CB067409 IQ36e02.x
34	847.5	40.3	501	2	BF464789	BF464789 UI-M-CG0P
35	847	40.2	483	1	AI325858	AI325858 mE89407.y
36	817	38.8	588	6	CD216600	CD216600 ppg2n.pk0
37	810.5	38.5	480	2	BE985750	BE985750 UI-M-CG0P
38	810.5	38.5	489	2	BE988426	BE988426 UI-M-CG0P
39	808	38.4	900	4	BG762138	BG762138 602717725
40	807	38.3	795	5	EX870688	EX870688 BX870688
41	800	38.0	531	7	CK903865	CK903865 1667406.x
42	800	38.0	534	4	BM052629	BM052629 1667406.x
43	791.5	37.6	484	2	AW435212	AW435212 UI-R-BJ0P
44	772	36.7	1394	4	BM451608	BM451608 AGENCOURT
45	768	36.5	842	9	AY410547	AY410547 Homo sapi

```
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
<1..>947
/locus_tag="KCNK3"
/locus_tag="HCM4297"

Alignment Scores:
Pred. No.: 1 09e-157 Length: 947
Score: 1631.50 Matches: 312
Percent Similarity: 99.68% Conservative: 1
Best Local Similarity: 99.36% Mismatches: 0
Query Match: 77.51% Indels: 1
DB: 9 Gaps: 1

ORIGIN
US-09-939-483-5 (1-405) x AY411659 (1-947)

QY 93 TyrGlyHisAlaAlaProSerThrAspGlyGlyLysValPheCysMetPheTyrAlaLeu 112
Db 3 TATGGTCATGCGCGCCACGACGAGCGAGGCAAGGTGTTCTGCATGTTCTACGGCGTG 62

QY 113 LeuGlyLeuProLeuThrLeuLeuMetPheGlnSerLeuGlyGluArgLeuThrPhe 132
Db 63 CTGGGCATCCGCTCACACTAGTATGTTCCAGAGCGCTGGGTGACGCATCAACACCTTC 122

QY 133 ValArgTyrLeuLeuHisArgAlaLysArgGlyLeuGlyMetArgHisAlaGluValSer 152
Db 123 GTGAGGTACTGTCGACCGTGCACAGAGGGGCTGGGCATGGCGACCGAGGTTGCTC 182

QY 153 MetAlaAsnMetValLeuLeuGlyPheValSerCysIleSerThrLeuCysIleGlyAla 172
Db 183 ATGCCCAACATGTGCTCATCGCTTCGTCGTGTCATCAGCAGCGTGTGCATCGCGCA 242

QY 173 AlaAlaPheSerTyrTyrGluArgTyrThrPhePheGlnAlaTyrTyrCysPheIle 192
Db 243 GCTGCCTTCTCTACTACGAGCGCTGAGCTTTCTCCAGGCTATTACTACTGCTTCATC 302

QY 193 ThrLeuThrThrIleGlyPheGlyAspTyrValAlaLeuGlnLysAspGlnAlaLeuGln 212
Db 303 ACCCTCACCAACATCGCTTCGGCGCATATGTGGCGCTGCAGAAGACCGAGGCGTGCAG 362

QY 213 ThrGlnProGlnTyrValAlaPheSerPheValTyrIleLeuThrGlyLeuThrValIle 232
Db 363 ACGCAGCGCAGATATGTGGCTTCAGCTTCGTGTACATCTCTACGCGCTCAGCGTCA 422

QY 233 GlyAlaPheLeuAsnLeuValValLeuArgPheMetThrMetAsnAlaGluAspGluLys 252
Db 423 GCGCGCTTCCTCAACCTCGTGGTGTGCGGATTCATGACCATGAACCGCGAGGACGAG 482

QY 253 ArgAspAlaGluHisArgAlaLeuLeuThrHisAsnGlyGlnAlaValGlyLeuGlyGly 272
Db 483 CGTGATCGGAGCACCAGCGCTTCGTCACGCAACAGCGCGAGCTGTGCGCTTGGGTGC 542

QY 273 LeuSerCysLeuSerGlySerLeuGlyAsp---ValArgProArgAspProValThrCys 291
Db 543 CTGAGCTGCTGAGCGGTAGCTGGCGGCGAGCGGTGGCTCCCGCGCACCCAGTCACATCG 602

QY 292 AlaAlaAlaGlyGlyValGlyValGlyValGlyValGlySerGlyPheArgAsnValTyr 311
Db 603 GCTGCGCGCGCGGAGCGGTGGCGGTGGCGGTGGCGGTGGCGGTGGCGGTGGCGGTAT 662

QY 312 AlaGluValLeuHisPheGlnSerMetCysSerCysLeuTyrTyrLysSerArgGluLys 331
Db 663 GCGCAGGTGCTGCATCTCCAGTCCATGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 722

QY 332 LeuGlnTyrSerIleProMetIleIleProArgAspLeuSerThrSerAspThrCysVal 351
Db 723 CTCAGTACTCTCATCCCATGATCATCCCGCGGACCTCTCCACGTCGACACCTCGGTG 782

QY 352 GluHisSerHisSerSerProGlyGlyGlyValGlyValGlyValGlyValGlyValPro 371
Db 783 GAGCAGACGACCTCGTGGCGGAGGCGGCGGCGCTACAGCGACACGCGCTTCACACCCC 842

QY 372 CysLeuCysSerGlyThrGlnArgSerAlaIleSerValSerValSerThrGlyLeuHisSer 391
Db 843 TGCCTGTGACGGGAGCGGAGCGGCTCGGCCATCAGCTGCTGTGCTGTGCTGTGCTGTG 902

QY 392 LeuAlaAlaPheArgGlyLeuMetLysArgArgSerSerVal 405
Db 903 CTGGCTGCTTCCGCGGCTCATGAAGCGCAGGAGCTCGGTG 944

RESULT 2
BC032047
LOCUS Mus musculus, clone IMAGE:4921810, mRNA. linear HTC 20-SEP-2002
DEFINITION BC032047
ACCESSION BC032047
VERSION BC032047.1 GI:21327815
KEYWORDS HTC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1043)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Gunnarane, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK plate: 31 Row: p Column: 15
This clone was selected for full length sequencing because it
passed the following selection criteria: Genomescan gene
prediction, Similarity but not identity to protein
This clone has the following problem: no polyA-tail.

FEATURES
Location/Qualifiers
1..1043
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4921810"
/tissue_type="Salivary gland, 10 week old female mouse"
/clone_lib="NCI CGAP_SG2"
/lab_host="DH105"
/note="Vector: pCMV-SPORT6"

ORIGIN
Alignment Scores:
Pred. No.: 4 4e-144 Length: 1043
Score: 1500.50 Matches: 292
Percent Similarity: 99.66% Conservative: 2
Best Local Similarity: 98.98% Mismatches: 0
Query Match: 71.28% Indels: 1
DB: 3 Gaps: 1

US-09-939-483-5 (1-405) x BC032047 (1-1043)

QY 1 GluAsnValArgThrLeuAlaLeuIleValCysThrPheThrLeuLeuValGlyAla 20
```



```
Db 157 CAGAAATGGCCAGCAGTTGGCTCTCATCTGTGTGCACCTTCACCTACCTGCTGCTGGCGGCC 216
Qy 21 AlaValPheAspAlaLeuGluSerGluProGluMetIleGluArgGlnArgLeuGluLeu 40
Db 217 GCGGTGTTCCGACGCACTGGAGTCGGAGCCGAGATGATCGAGCGCAGCGCTGAGCGT 276
Qy 41 ArgGlnLeuGluLeuArgAlaArgTyrAsnLeuSerGluGlyGlyTyrGluLeuGluLeu 60
Db 277 CGGAGCTGGAGCTGCGGCGCGCTACAACTTCAGCAGGCGCGCTACGAGGAGCTGGAG 336
Qy 61 ArgValValLeuArgLeuLeuPheHisLysAlaGlyValGlnTyrArgPheAlaGlySer 80
Db 337 GCGGTGCTGCGCTCAAGCCGACAGCGCGCGCTGCGAGTGCAGTGGCGCTTCGCGCGTCC 396
Qy 81 PheTyrPheAlaIleThrValIleThrThrIleGlyTyrGlyHisAlaAlaProSerThr 100
Db 397 TTCTACTTGGCCATCAGCGTCATCACCACCATCGCTATGCTATGCTATGCTGCGCGCCAGCAG 456
Qy 101 AspGlyGlyLysValPheCysMetPheTyrAlaLeuLeuGlyIleProLeuThrLeuIle 120
Db 457 GACGGAGCGCAAGGTGTTCTGCACTGTTCTACGCGCTGCTGGGCAATCCCGCTCACACTAGTC 516
Qy 121 MetPheGlnSerLeuGlyGluArgIleAsnThrPheValArgTyrLeuLeuHisArgAla 140
Db 517 ATGTTCCAGAGCCTGGGTGAACGATCAACACCTTCGTGAGGTACCTGCTGCACCGTGC 576
Qy 141 LysArgGlyLeuGlyMetArgHisAlaGluValSerMetAlaAsnMetValLeuIleGly 160
Db 577 AAGAGGGGCTGGCATCGGCAGCGAGGTGTCATGGCCACATGGTGTCTCATCGT 636
Qy 161 PheValSerCysIleSerThrLeuCysIleGlyAlaAlaPheSerTyrTyrGluArg 180
Db 637 TTCGTGTCGTGCATCAGCAGCAGCTGTGCATCGCGCAGCTGCTCTCTACTACGAGCGC 696
Qy 181 TrpThrPhePheGlnAlaTyrTyrCysPheIleThrLeuThrThrIleGlyPheGly 200
Db 697 TGGACTTCTTCAGAGCCTATTACTGCTTTCATCACCCTCCACCATCGGCTTCGCG 756
Qy 201 AspTyrValAlaLeuGlnLysAspGlnAlaLeuGlnThrGlnProGlnTyrValAlaPhe 220
Db 757 GACTATGTGGCGCTGCAGAGGACCGCGCTGCAGAGCGAGCGCAGTATGTGGCCTTC 816
Qy 221 SerPheValTyrIleLeuThrGlyLeuThrValIleGlyAlaPheLeuAsnLeuVal 240
Db 817 AGCTTCGTGTACATCTCACGGGCTCACGGTCTATCGCGCTTCTCTCAACCTCGTGGT 876
Qy 241 LeuArgPheMetThrMetAsnAlaGluAspGlyLysArgAspAlaGluHisArgAlaLeu 260
Db 877 CTGCGATTATGACCATGAACCGCGAGGACGAGAGCGGTGATGCGGAGCACCGCGCCTG 936
Qy 261 LeuThrHisAsnGlyGlnAlaValGlyLeuGlyLeuSerCysLeuSerGlySerLeu 280
Db 937 CTCAGCAGCAACGCGCAGGCTGTGGCTGGTGGCTGAGTGCCTGAGCGGTAGGCTG 996
Qy 281 GlyAsp---ValArgProArgAspProValThrCysAlaAlaAla 294
Db 997 GCGCAGCGCGTGGCTCCCGCGACCCAGTCACATGCTGCGGCC 1041

RESULT 3
AY411657
LOCUS
DEFINITION Homo sapiens KCNK3 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY411657
VERSION AY411657.1 GI:39767625
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 902)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
```

```
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
JOURNAL PUBMED 14671302
REFERENCE 2 (bases 1 to 902)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source 1..902
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..>902
/genes="KCNK3"
/locus_tag="HCM4297"
ORIGIN
Alignment Scores:
Pred. No.: 6,79e-131 Length: 902
Score: 1372.00 Matches: 269
Percent Similarity: 87.86% Conservatve: 6
Best Local Similarity: 85.94% Mismatches: 24
Query Match: 65.18% Indels: 14
DB: 9 Gaps: 2
US-09-939-483-5 (1-405) x AY411657 (1-902)
Qy 93 TyrGlyHisAlaAlaProSerThrAspGlyGlyLysValPheCysMetPheTyrAlaLeu 112
Db 3 TACGGCAGCGCGCACCCAGCAGCATGGCGCAAGGTGTTCTGCATGTTCTACGCGCTG 62
Qy 113 LeuGlyIleProLeuThrLeuIleMetPheGlnSerLeuGlyGluArgIleAsnThrPhe 132
Db 63 CTGGGCATCCGCTCAGCTCGTCATGTTCCAGAGCCTGGCGCAGCATCAACACCTTG 122
Qy 133 ValArgTyrLeuLeuHisArgAlaLysArgGlyLysMetArgHisAlaGluValSer 152
Db 123 GTGAGGTACTGTGTGACCGCGCCAGAGAGGGGCTGGGCATGGCGCGCGACGTGCC 182
Qy 153 MetAlaAsnMetValLeuIleGlyPheValSerCysIleSerThrLeuCysIleGlyAla 172
Db 183 ATGCCCAACATGCTGCTCATCGGCTTCTTCTGTCATCAGCACGCTGTGTCATCGCGCC 242
Qy 173 AlaAlaPheSerTyrTyrGluArgTyrThrPhePheGlnAlaTyrTyrCysPheIle 192
Db 243 GCGCGCTTCTCCCACTACGAGCATCTGACCTTCTTCCAGCGCTACTACTACTGCTCATC 302
Qy 193 ThrLeuThrThrIleGlyPheGlyAspTyrValAlaLeuGlnLysAspGlnAlaLeuGln 212
Db 303 ACCCTCACCAACATCGGCTTCGGCGACTACGTGGCGCTGCAGAGGACCGCGCTGCAG 362
Qy 213 ThrGlnProGlnTyrValAlaPheSerPheValTyrIleLeuThrGlyLeuThrValIle 232
Db 363 ACGCAGCGCGCAGTACGTGGCGCTTTCAGCTTCGTCTACATCTTACCGGCTCTACGGTCA 422
Qy 233 GlyAlaPheLeuAsnLeuValLeuArgPheMetThrMetAsnAlaGluAspGlyLys 252
Db 423 GCGCGCTTCTCAACCTCGGTGGTGGCTTCATGACCATGAACCGCGGAGGACGAGAAG 482
Qy 253 ArgAspAlaGluHisArgAlaLeuLeuThrHisAsnGlyGlnAlaValGlyLeuGly 272
Db 483 CGCGACCGCGAGCACCGCGCGCTGCTCACGCGCAACGGGCGAGCGCGCGCGGAGGG 542
```

Qy 273 LeuSerCysLeuSerGlySerLeuGlyValArgProArgAspProValThrCysAla 292
 Db 543 -----GGTGGCAGCGCGCACACACTAGGACACCGCCTCATCCAG 591
 Qy 293 AlaAlaAlaGlyValGlyValGlyValGlySerGlyPheArgAsnValTyrAla 312
 Db 582 GCGGCACGC-----GGCGGCGCGCGCTTCGCAACGCTACGCG 620
 Qy 313 GluValLeuHisPheGlnSerMetCysSerCysLeuTrpTyrIysSerArgGluLysLeu 332
 Db 621 GAGGTGTCGACATTCAGATTCATGTCTGCTGTGTGTACAGAGCGCGAGAGCTG 680
 Qy 333 GlnTyrSerIleProMetIleIleProArgAspLeuSerThrSerAspThrCysValGlu 352
 Db 681 CAGTACTCCATCCCATGATCATCCCGCGGAGACTCTCCACGTCACACGTCGCTGGAG 740
 Qy 353 HisSerHisSerProGlyGlyGlyArgTyrSerAspThrProSerHisProCys 372
 Db 741 CAGAGCCACTCGTCGCGCGGAGGCGCGCGCTACAGCAGACACGCGCTCGCAGCGCTGC 800
 Qy 373 LeuCysSerGlyThrGlnArgSerAlaIleSerSerValSerThrGlyLeuHisSerLeu 392
 Db 801 CTGTGACGCGGCGCGCCACGCTCCGCGCATCAGTCTCGGTGTCCACGGTCTGCACGCTG 860
 Qy 393 AlaAlaPheArgGlyLeuMetLysArgArgSerSerVal 405
 Db 861 TCACACCTTCGCGCGCCTCATGAGCGCAGAGATCCGCTG 899

RESULT 4

LOCUS BX359243 1045 bp mRNA linear EST 08-APR-2004
 DEFINITION BX359243 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 clone CS0D1055YC13 5-PRIME, mRNA sequence.
 ACCESSION BX359243
 VERSION BX359243.2 GI:46303841
 SOURCE EST.
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1. (bases 1 to 1045)
 Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On May 5, 2003 this sequence version replaced gi:30374332.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 1453.f
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?s=CS0D1055AB07QP1&c=1453.f.

FEATURES

source Location/Qualifiers
 1..1045
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D1055YC13"
 /issue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /notes="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores: 5.17e-122 Length: 1045
 Pred. No.:

Score: 1287.00 Matches: 249
 Percent Similarity: 96.25% Conservatives: 8
 Best Local Similarity: 93.26% Mismatches: 10
 Query Match: 61.14% Indels: 0
 DB: 5 Gaps: 0

US-09-939-483-5 (1-405) x BX359243 (1-1045)

Qy 1 GluAsnValArgThrLeuAlaLeuIleValCysThrPheThrTyrLeuLeuValGlyAla 20
 Db 170 CAGAAAGTCGCGACGCTGGCGCTCATCGTGTGCACCTTCCACCTACCTGCTGGTGGCGGC 229
 Qy 21 AlaValPheAspAlaLeuGluSerGluProGluMetIleGluArgGlnArgLeuGluLeu 40
 Db 230 GCGGTCTTCGAGCGCTGGAGTCGGAGCCGAGCTGATCGAGCGGAGGCTTCGAGCTG 289
 Qy 41 ArgGlnLeuGluLeuArgAlaArgTyrAsnLeuSerGluGlyTyrGluGluLeuGlu 60
 Db 290 CGGCAGCAGAGAGCTCGGCGCGCTACAACTCAGCAGGCGCGCTACGAGGAGCTGGAG 349
 Qy 61 ArgValValLeuArgLeuLysProHisLysAlaGlyValGlnTrpArgPheAlaGlySer 80
 Db 350 CCGCTCGTCTCGCGCTCAAGCGCGCACAGGCGCGCTGACGTGGCGCTTCGCGGCTCC 409
 Qy 81 PheTyrPheAlaIleThrValIleThrIleGlyTyrGlyHisAlaAlaProSerThr 100
 Db 410 TTCTACTTCGCCATCACCCTCATCCACCATCGGCTACGGGCACCGGCACCCAGCAGC 469
 Qy 101 AspGlyGlyLysValPheCysMetPheTyrAlaLeuLeuGlyIleProLeuThrLeuIle 120
 Db 470 GATGCGCGCAAGGTGCTGTGCTGTCTACGCGCTGCTGGGCATCCCGCTCACGCTCGTC 529
 Qy 121 MetPheGlnSerLeuGlyGluArgIleAsnThrPheValArgTyrLeuLeuHisArgAla 140
 Db 530 ATGTTCCAGAGCTCGGCGAGCGCATCAACACTTGGTGGGTACTGCTGCACCGCGCC 589
 Qy 141 LysArgGlyLeuGlyMetArgHisAlaGluValSerMetAlaAsnMetValLeuIleGly 160
 Db 590 AAGAGGGGCTGGGATGCGGCGCGCGGACGTGTCTATGGCCAAATAGTGTCTCATCGGC 649
 Qy 161 PheValSerCysIleSerThrLeuCysIleGlyAlaAlaAlaPheSerTyrTyrGluArg 180
 Db 650 TTCTTCTCGTGCATCAGCAGCTTGTGCATCGGCGCGCGCTTCTCCACTACGAGCAC 709
 Qy 181 TrpThrPhePheGlnAlaTyrTyrCysPheIleThrLeuThrThrIleGlyPheGly 200
 Db 710 TGGACCTTCTTCAGGCGCTTACTACTGCTTCATCACCCCTCACCACCATCGGCTTCGGC 769
 Qy 201 AspTyrValAlaLeuGlnLysAspGlnAlaLeuGlnThrGlnProGlnTyrValAlaPhe 220
 Db 770 GACTACGTGGCGCTGCAGAGGACCGGCGCTGCAGAGCGCAGCGCTACGTGGCCTTC 829
 Qy 221 SerPheValTyrIleLeuThrGlyLeuThrValIleGlyAlaPheLeuAsnLeuValVal 240
 Db 830 AGCTTCGTCTACATCTTACGGGCGCTCAGGTCATCGGCGCTTCTCAACCTCGTGGTG 889
 Qy 241 LeuArgPheMetThrMetAsnAlaGluAspGluLysArgAspAlaGluHisArgAlaLeu 260
 Db 890 CTGCGCTTCATGACCATGAAGCGGAGGACGAGAGCGCGGAGCGGAGCAGCGCGCTG 949
 Qy 261 LeuThrHisAsnGlyGlnAla 267
 Db 950 CTCAMGCCAAGGCGCAGCGG 970

RESULT 5

AY411658
 LOCUS Pan troglodytes KCNK3 gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.
 DEFINITION AY411658
 ACCESSION AY411658.1 GI:39767626
 VERSION GSS.
 KEYWORDS Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 REFERENCE 1 (bases 1 to 874)
 AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D. and Cargill, M.
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 874)
 AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D. and Cargill, M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
 FEATURES
 source
 1..874
 /organism="Pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
 gene
 <1..>874
 /gene="KCNK3"
 /locus_tag="HCMA297"
 ORIGIN
 Alignment Scores:
 Pred. No.: 2.66e-121 Length: 874
 Score: 1279.00 Matches: 251
 Percent Similarity: 84.54% Conservative: 6
 Best Local Similarity: 82.57% Mismatches: 33
 Query Match: 60.76% Indels: 14
 DB: 9 Gaps: 2
 US-09-939-483-5 (1-405) x AV411658 (1-874)
 Qy 93 TyrGlyHisAlaAlaProSerThrAspGlyLysValPheCysMetPheTyrAlaLeu 112
 Db 3 TACGGCAGCGCGCGCCAGCACGAGTGGCGGAAGGTGTCTGCATGTTCTACGCGCTG 62
 Qy 113 LeuGlyIleProLeuThrLeuIleMetPheGlnSerLeuGlyGluArgIleAsnThrPhe 132
 Db 63 CTGGGCATCCCGCTCAGCTCGTCTGTCATGTTCCAGAGCTGGCGGAGCGATCAACACCTTG 122
 Qy 133 ValArgTyrLeuLeuHisArgAlaLysArgGlyLeuGlyMetArgHisAlaGluValSer 152
 Db 123 GTGAGGTACCTGCTGCACCGCGCCAGCAAGAGGGCTGGGCATGGCGCGCGAGCTGCC 182
 Qy 153 MetAlaIleMetValLeuIleGlyPheValSerCysIleSerThrLeuCysIleGlyAla 172
 Db 183 ATGGCCACATGATGGTCTCATCGGCTCTCTCTGTCGTCATCAGACGCTGTGTCATCGGCGC 242
 Qy 173 AlaAlaPheSerTyrTyrGluArgTyrThrPheGlnAlaTyrTyrCysPheIle 192
 Db 243 GCCGCTTCTCCACTACGACACTGGACCTCTTCAGGGCTACTACTACTGCTTCATC 302
 Qy 193 ThrLeuThrThrIleGlyPheGlyAspTyrValAlaLeuGlnLysAspGlnAlaLeuGln 212
 Db 303 ACGCTCACCATCGCTTCGGCGACTACGTGGCGTGCAGAGGACCGAGCCCTCGAG 362
 Qy 213 ThrGlnProGlnTyrValAlaPheSerPheValTyrIleLeuThrGlyLeuThrValIle 232
 Db 363 ACGCAGCGCGATGATGGTCTCAGCTTCTGCTCTACATCTCTTACGGGCTCCACGGCTCATC 422
 Qy 233 GlyAlaPheLeuAsnLeuValValLeuArgPheMetThrMetAsnAlaGluAspGluLys 252
 Db 423 GCGCGCTTCTCTCAACCTCGTGGTGTGCGCTTCATGACCATGAACGCGGAGGACGAGAAG 482

Qy 253 ArgAspAlaGluHisArgAlaLeuLeuThrHisAspGlyGlnAlaValGlyLeuGlyGly 272
 Db 483 CGCGAGCGCGCAGCACCGCGCTGCTCAGCGCAACGCGGCGCGCGCGCGCGAGGG 542
 Qy 273 LeuSerCysLeuSerGlySerLeuGlyAspValArgProArgAspProValThrCysAla 292
 Db 543 -----AGTGGAGCGCGCCACACATACGACACCGCGCTCATCCACG 581
 Qy 293 AlaAlaAlaGlyValGlyValGlyValGlyValGlyValGlyValGlyValGlyVal 312
 Db 582 GCGGCGAGCG-----GGCGCGCGCGCTTCCGCAACGCTTACGCG 620
 Qy 313 GluValLeuHisPheGlnSerMetCysSerCysLeuTyrTyrIleSerArgGluLysLeu 332
 Db 621 GAGGTGCTGCATCTCCAGTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 680
 Qy 333 GlnTyrSerIleProMetIleIleProArgAspLeuSerThrSerAspThrCysValGlu 352
 Db 681 CAGTACTCCATCCCATGATCATCCCGGAGACTCTCCACGTCGACACGTCGCTGGAG 740
 Qy 353 HisSerHisSerSerProGlyGlyGlyArgTyrSerAspThrProSerHisProCys 372
 Db 741 CAGAGCCACTCGTGGCGGAGGGCGCGCTANANCGACACGNNNCGCGACGCTGC 800
 Qy 373 LeuCysSerGlyThrGlnArgSerAlaIleSerSerValSerThrGlyLeuHisSerLeu 392
 Db 801 CTGTGNANCGGGCGCGCACGCTCCGCCATNNNCTCGGTGTCCACGGGTGTGCACANCTG 860
 Qy 393 AlaAlaPheArg 396
 Db 861 TCCACCTTCGCG 872
 RESULT 6
 BI412471
 LOCUS
 DEFINITION 995 bp mRNA linear EST 14-AUG-2001
 602985964F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5142374 5',
 mRNA sequence.
 BI412471
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 995)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LLM11350 row: 0 column: 15
 High quality sequence start: 3
 High quality sequence stop: 927.
 Location/Qualifiers
 1..995
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="CZECH II"
 /db_xref="taxon:10090"
 /clone="IMAGE:5142374"
 /tissue_type="pooled lung tumors"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NCI_CGAP_Lu33"
 /notes="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a

modified polylinker; Site 1: NotI; Site 2: EcoRI; 1st strand cDNA was prepared from mRNA obtained from pooled lung tumors with a Not I - oligo(dT) primer [5'-TGTTACCAATCTCAAGTGGGAGCGCGCTCTGTTTCTTTTCTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Alignment Scores:
 Pred. No.: 8.32e-118 Length: 995
 Score: 1246.00 Matches: 733
 Percent Similarity: 93.65% Conservative: 7
 Best Local Similarity: 91.30% Mismatches: 9
 Query Match: 59.19% Indels: 12
 DB: 4 Gaps: 2

US-09-939-483-5 (1-405) x BI412471 (1-995)

QY 1 GluAsnValArgThrLeuAlaLeuValCysThrPheThrTyrLeuLeuValGlyAla 20
 Db 117 CAGAAATGGCGACGTTGGCTCTCATCGTGTGCACCTTACCTGCTGGTGGCGCC 176
 QY 21 AlaValPheAspAlaLeuGluSerGluProGluMetIleGluArgGlnArgLeuLeu 40
 Db 177 GCGGTGTTCAGCGCACTGGAGTGGAGCGGAGATGATCGAGCGGACGGCTGGAGCTG 236
 QY 41 ArgGlnLeuGluLeuArgAlaArgTyrAsnLeuSerGluGlyTyrGluGluLeuGlu 60
 Db 237 CGGCAGCTGAGCTGCGGGCGCGCTACACCTCAGCGAGGCGGCTACGAGGAGCTGGAG 296
 QY 61 ArgValValLeuArgLeuLysProHisLysAlaGlyValGlnTrpArgPheAlaGlySer 80
 Db 297 CGCGTGTGTGGCGCTCAAGCGCGCAATGCGCGGCGTGCAGTGGCGCTTCGCGCGCTCC 356
 QY 81 PheTyrPheAlaIleThrValIleThrIleGlyTyrGlyHisAlaAlaProSerThr 100
 Db 357 TTCTACTTCCCATCACCCTCATCACCATCGCTATGCTATGCTATGCTGCGGCGCCACG 416
 QY 101 AspGlyLysValPheCysMetPheTyrAlaLeuLeuGlyLeuProLeuThrLeuIle 120
 Db 417 GACGGAGCGCAAGGTGTTCTCATGCTGTGCGGCTGCTGGGCTCCCGCTCATCAGTATC 476
 QY 121 MetPheGlnSerLeuGlyGluArgIleAsnThrPheValArgTyrLeuLeuHisArgAla 140
 Db 477 ATGTTCCAGAGCGCTGGGTGAACGCATCAACACCTTGTGAGGTACCTGCTGCACCGTGC 536
 QY 141 LysArgGlyLeuGlyMetArgHisAlaGluValSerMetAlaAsnMetValLeuIleGly 160
 Db 537 AACAGGGGGTGGGCATGCGGCGCGGAGGTTCATATGCGCAACATGTGCTCATCGGT 596
 QY 161 PheValSerCysIleSerThrLeuCysIleGlyAlaAlaAlaPheSerTyrTyrGluArg 180
 Db 597 TTCGTGCGGTGCATCAGCAGCGTGTGCATCGGCGAGCTGCTTCTTCTACTACGAGCGC 656
 QY 181 TrpThrPhePheGlnAlaTyrTyrCysPheIleThrLeuThrThrIleGlyPheGly 200
 Db 657 TGCAGCTTCTTCAGGCGCTTACTACTGCTTTCATCACCCTCAC-ACCATCGGCTTCGGC 715
 QY 201 AspTyrVal-AlaLeuGlnLysAspGlnAlaLeuGlnThrGlnProGlnTyrValAla-P 220
 Db 716 GACTATGTGGCGCTGCAGAGGACCGCGCTGCAGCGCAGCG-CAGTATGTGGCCCT 774
 QY 220 heSerPhe-ValTyrIleLeuThrGlyLeu-ThrValIleGlyAlaPheLeuAsnLeuVa 239
 Db 775 TCAGCTTCGGTGTACATCCTCAGCGGCGCTCAACGGGTCAATCGGCGCTTCTCAACCTCGT 834
 QY 239 lValLeuArgPhe-MetThrMetAsnAlaGluAspGluLysArgAsp-AlaGluHisArg 258
 Db 835 GGTGCTCGGATTATTGACCATGAACGCCGAGGACGAGAGCGTGAATGCGGAGCCCGG 894

QY 259 -AlaLeuLeuThrHis-AsnGlyGlnAlaValGlyLeu---GlyGlyLeuSerCysLeuS 277
 Db 895 GGCCTTCTCAGCACAAACGCGAGGCTGTGGCTGTGGCTGTGAGACTTGTCTTAA 954
 QY 277 exGlySerLeuGlyAsp---ValArgProArgAspProVal 289
 Db 955 CGGGTAGCTGGCGGACGCGTTCGTCCGAAACCAAGT 995
 RESULT 7
 CK602460
 LOCUS
 DEFINITION
 AGENCOURT 17898437 NIH_MGC.234 Rattus norvegicus cDNA clone
 IMAGE:7192291 5', mRNA sequence.
 ACCESSION
 CK602460
 VERSION
 CK602460.1 GI:41115757
 KEYWORDS
 EST.
 SOURCE
 Rattus norvegicus (Norway rat)
 ORGANISM
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 789)
 REFERENCE
 NIH-MGC http://mgc.nci.nih.gov/.
 AUTHORS
 National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE
 Unpublished (1999)
 JOURNAL
 COMMENT
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 M0A07 Bethesda, MD 20892
 Email: cgapbs-r@mail.nih.gov
 Tissue procurement: Howard Jacobs
 cDNA Library preparation: Express Genomics
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM15052 row: 1 column: 17
 High quality sequence stop: 654.
 FEATURES
 Location/Qualifiers
 1..789
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /db_xref="taxon:10116"
 /clone="IMAGE:7192291"
 /tissue_type="heart, pooled"
 /lab_host="DH10B Tona"
 /clone_lib="NIH_MGC_234"
 /note="Organ: heart; Vector: pExpress-1; Site 1: EcoRV;
 Site 2: NotI; RNA obtained from pooled heart tissue from a
 mix of male and female animals at 8 wk old. Tissues were
 snap-frozen and kept at -80C for two days before RNA
 extraction and purification (Tri-reagent method). cDNA was
 primed using oligo-dT primer:
 5'-pCAGTAGTCTAGATCGGAGCGGCCCT(7)25-3' and cloned into
 the EcoRV/NotI sites of pExpress-1. Size-selection >1.4kb
 resulted in an average insert size of 2.2 kb. This primary
 library is normalized (non-normalized primary library is
 NIH_MGC_233) and was constructed by Express Genomics
 (Frederick, MD). Note: this is a NIH_MGC library."
 ORIGIN
 Alignment Scores:
 Pred. No.: 2.65e-116 Length: 789
 Score: 1230.00 Matches: 237
 Percent Similarity: 98.76% Conservative: 1
 Best Local Similarity: 99.34% Mismatches: 3
 Query Match: 58.43% Indels: 0
 DB: 7 Gaps: 0
 US-09-939-483-5 (1-405) x CK602460 (1-789)
 QY 35 ArgGlnArgLeuGluLeuArgGlnLeuGluLeuArgAlaArgTyrAsnLeuSerGluGly 54

```

Db 1 CGGCGGCGCTGGAGCTGCGGCACTGGAGCTGCGGCGCGCTACACCTCAGGAGGC 60
Qy 55 GlyTyrGluGluGluArgValValLeuArgLeuLysProHisLysAlaGlyValGln 74
Db 61 GGCTACGAGGAGCTGGAGCGCTGCTGCTGCGCTCAAGCGCACAGGCGGCGTCGAG 120
Qy 75 TrpArgPheAlaGlySerPheTyrPheAlaIleThrValIleThrThrIleGlyTyrGly 94
Db 121 TGGCGCTTCGCGCGCTCTCTTCTACTTCGCCATCACTCCGTCATCACCAATCGGCTATGGT 180
Qy 95 HisAlaAlaProSerThrAspGlyGlyLysValPheCysMetPheTyrAlaLeuLeuGly 114
Db 181 CATCGCGCTCCACACGAGCGAGGCAAGTGTTCTGCATGTTCTACGCGCTGCTGGC 240
Qy 115 IleProLeuThrLeuIleMetPheGlnSerLeuGlyGluArgIleAsnThrPheValArg 134
Db 241 ATCCCGCTCACACTAGTCATGTTCCAGAGCGCTGGGTGAACGATCAACACTTCGTGAGG 300
Qy 135 TyrLeuLeuHisArgAlaLysArgGlyLeuGlyMetArgHisAlaGluValSerMetAla 154
Db 301 TACCTGTGCACCGTGGCAAGAGGGGCTGGGCATGCGGCACGCGGAGGTGTCCATGGCC 360
Qy 155 AsnMetValLeuIleGlyPheValSerCysIleSerThrLeuCysIleGlyAlaAlaAla 174
Db 361 AACATGTTGCTCATCGTTTCTGTTGTCGTGATCAGCACGCTGTGTATCGGCGCGCTGCC 420
Qy 175 PheSerTyrTyrGluArgTyrPhePheGlnAlaTyrTyrCysPheIleThrLeu 194
Db 421 TTCTCTTACTATGAGCGCTGGACTTCTTCCAGGCGCTTACTTACTTCTTCATCACCGCTC 480
Qy 195 ThrThrIleGlyPheGlyAspTyrValAlaLeuGlnLysAspGlnAlaLeuGlnThrGln 214
Db 481 ACCACCATCGCTTCGCGCGACTAGCTGGCGCTGCAGAGGACCAAGCGCTGCAACGCGAG 540
Qy 215 ProGlnTyrValAlaPheSerPheValTyrIleLeuThrGlyLeuThrValIleGlyAla 234
Db 541 CCTCAGTACGTGGCTTCAGCTTCGTATACATCTCCACCGCGCTTCACGGTATCGGCGCC 600
Qy 235 PheLeuAsnLeuValValLeuArgPheMetThrMetAsnAlaGluAspGluLysArgAsp 254
Db 601 TTCCTCAACCTCGTGGTGTGCGATTTCATGACCATGAACCGCGAGGACGAGAGCGTAT 660
Qy 255 AlaGluHisArgAlaLeuLeuThrHisAsnGlyGlnAlaValGlyLeuGlyLeuSer 274
Db 661 GCAGAGCACCGTGGCTGCTCACGACAATGGCCAGCTGGCGCGCTGGGTGGCGCTGAGC 720
Qy 275 Cys 275
Db 721 TGC 723

RESULT 8
BG750477
LOCUS BG750477 881 bp mRNA linear EST 15-MAY-2001
DEFINITION 602709342F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4845658 5',
mRNA sequence.
ACCESSION BG750477
VERSION BG750477.1 GI:14061130
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 881)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

```

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLCM1685 row: d column: 11
High quality sequence stop: 804.

FEATURES
Location/Qualifiers
source
1..881
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4845658"
/tissue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_43"
/notes="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library. |"

ORIGIN

Alignment Scores: 2,54e-111 Length: 881
Pred. No.: 1182.50 Matches: 251
Score: 83.82% Conservative: 8
Percent Similarity: 81.23% Mismatches: 34
Best Local Similarity: 56.18% Indels: 19
Query Match: 4 Gaps: 2
DB:

US-09-939-483-5 (1-405) x BG750477 (1-881)

Qy 87 ValIleThrThrIleGlyTyrGlyHisAlaAlaProSerThrAspGlyGlyLysValPhe 106
Db 2 GTTCATCACCACTCCGCTACGGGACCGGACCCAGCAGCATGGAGTGGCGCAGGTTC 61

Qy 107 CysMetPheTyrAlaLeuLeuGlyIleProLeuThrLeuIleMetPheGlnSerLeuGly 126
Db 62 TGCATGTTCTACGCGCTGCTGGGCATCCGCTCACGCTCGTCTATGTTCCAGAGCTGGGC 121

Qy 127 GluArgIleAsnThrPheValArgTyrLeuLeuHisArgAlaLysArgGlyLeuGlyMet 146
Db 122 GAGCGCATCAACACTTGTGTAGGTACCTGCTGCACCGCGCCCAAGAGGCGCTGGGCATG 181

Qy 147 ArgHisAlaGluValSerMetAlaAsnMetValLeuIleGlyPheValSerCysIleSer 166
Db 182 CGGCGCGCGAGCGTGTCCATGCCAACATGGTGTCTCATCGGCTTCTCTCGTCATCAGC 241

Qy 167 ThrLeuCysIleGlyAlaAlaPheSerTyrTyrGluArgTyrThrPhePheGlnAla 186
Db 242 AGCGTGTGCATGGCGCGCGCTTCTCCACTAGCAGCAGCTGGACCTTCTTCCAGGCC 301

Qy 187 TyrTyrTyrCysPheIleThrIleThrIleGlyPheGlyAspTyrValAlaLeuGln 206
Db 302 TACTACTACTGCTTTCATCCCTCACCATCGGCTTCGGCGACTACGCTGGCGCTGCAG 361

Qy 207 LysAsp-GlnAlaLeuGlnThrGlnProGlnTyrValAlaPheSerPheValTyrIleLe 226
Db 362 AGGACATAGGCGCTGCACAGCGCGCGAGTACGTGGCGCTTCAGCTTCTGTCTACATCCT 421

Qy 226 uThrGlyLeuThrValIleGlyAlaPheLeuAsnLeuValValLeuArgPheMetThrMe 246
Db 422 TACGGCGCTCACGGTTCATCGGCGCTTCTCAACCTCGTGGTGTCTGGCTTTCATGACCAT 481

Qy 246 tAsnAlaGluAspGluLysArgAspAlaGluHisArgAlaLeuLeuThrHisAsnGlyG 266
Db 482 GAACGCGCGAGGACGAGAGCGAGCGACCGCGCGCTGCTCACGCGCAACCGGCA 541

Qy 266 nAlaValGlyLeuGlyGlyLeuSerCysLeuSerGlySerLeuGlyAspValArgProAr 286
Db 542 GCGCGCGCGCGCGGAGGG-----GGTGGCAGCGCGCACACTAC 580

Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Fape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, E., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (infoimage.llnl.gov) for further information.
This read is a RESSEQUENCE of a previously sequenced mouse clone
This read has been verified (found to hit its original self in the correct orientation)
Possible reversed clone: similarity on wrong strand
MG1:20655
Seq primer: -40RP from Gibco
High quality sequence stop: 463
POLYA=No.

FEATURES

Location/Qualifiers

1..677
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:303895"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares mouse pJNMF19.5"
/note="Vector: pRT3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCCATTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRT3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Patima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."

ORIGIN

Alignment Scores:

Pred. No.: 1.1e-106 Length: 677
Score: 1136.00 Matches: 221
Percent Similarity: 98.67% Conservatave: 1
Best Local Similarity: 98.22% Mismatches: 3
Query Match: 53.97% Indels: 0
DB: 1 Gaps: 0

US-09-939-483-5 (1-405) x AI605559 (1-677)

Qy 2 AsnValArgThrLeuAlaLeuLeuValCysThrPheThrTyrLeuLeuValGlyAlaAla 21
Db 3 AATGTGGCAGCTTGGCTCTCATCGTGTGCACCTTACCTACCTGTGTGGTGGCGCGCG 62
Qy 22 ValPheAlaLeuLeuSerGluProGluMetIleGluArgGlnArgLeuGluLeuArg 41
Db 63 GTGTTCAGCGCAGCTGGAGTCGGAGCCGGAGATGATCGAGCGCGAGCGGTGAGCTCGG 122
Qy 42 GlnLeuGluLeuArgAlaAATGTYrAsnLeuSerGluGlyGlyTyrGluGluLeuGluArg 61
Db 123 CAGCTGGAGCTCGCGCGCGCTACACCTCAGCGAGCGCGGTACGAGGAGCTGAGCGCG 182
Qy 62 ValValLeuArgLeuLeuProHisLysAlaGlyValGlnTrpArgPheAlaGlySerPhe 81
Db 183 GTCTGTGTCTCGCTCAAGCCGCAAGCGCGGTGCGAGTGGCGCTTCGCGGCTCTTC 242
Qy 82 TyrPheAlaIleThrValIleThrThrIleGlyTyrGlyHisAlaAlaProSerThrAsp 101
Db 243 TACTTTCGCCATCACCCTGATCACCACCATCGGCTATGTGTATCGCGCGCCCGCAGCGGAC 302

Qy 102 GlyGlyLysValPheCysMetPheTyrAlaLeuLeuGlyIleProLeuThrLeuIleMet 121
Db 303 GGAGGCAAGGTGTTCTGTCATGTTCTACGGCGCTCTGGGCATCCCGCTCACAGTAGTCATG 362
Qy 122 PheGlnSerLeuGlyGluArgIleAsnThrPheValArgTyrLeuLeuHisArgAlaLys 141
Db 363 TTCAGAGCCTGGGTGAACGATCAACACCTTCGTGAGGTACCTGCTGCACCGTGCACAG 422
Qy 142 ArgGlyLeuGlyMetArgHisAlaGluValSerMetAlaAsnMetValLeuIleGlyPhe 161
Db 423 AGGGGCTGGGCATCGGCACGCGAGGTGTCCATGGCCAAACATGTGTCTCATCGGTTTC 482
Qy 162 ValSerCysIleSerThrLeuCysIleGlyAlaAlaAlaPheSerTyrTyrGluArgTrp 181
Db 483 GTCTGTGTCATCAGCAGCTGTGCATCGCGCAGCTGCCTTCTCTACTACGAGCGGTGG 542
Qy 182 ThrPhePheGlnAlaTyrTyrTyrCysPheIleThrLeuThrThrIleGlyPheGlyAsp 201
Db 543 ACTTTCCTTCAGGCTTATTACTACTGCTTCATCACCTTCACCACTCGGCTTCGGCGAC 602
Qy 202 TyrValAlaLeuGlnLysAspGlnAlaLeuGlnThrGlnProGlnTyrValAlaPheSer 221
Db 603 TATGTGGCGCTGCAGAGGACGAGCGCTGCACAGCGCAGCAGCATGTGGCTTCAGC 662
Qy 222 PheValTyrIleLeu 226
Db 663 TTCGTGTACATCCTN 677
RESULT 11
BX922107
LOCUS
DEFINITION
BX922107 Sus Scrofa library (scan) Sus scrofa cDNA clone
scan0024d.b.23 5prim, mRNA sequence.
ACCESSION
BX922107
VERSION
BX922107.1 GI:41138955
KEYWORDS
EST.
SOURCE
Sus scrofa (pig)
ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
1 (bases 1 to 725)
Bonnert, A., Tosser-Klopp, G., Beine, F., Cabau, C., Villegier, S.,
Soares, M., Bonaldo, F. and Hately, F.
A Pig Normalised Multi-Tissue cDNA Library
Unpublished (2003)
Contact: Tosser-Klopp G
Genetique Animale
Institut National de la Recherche Agronomique
Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
cedex, FRANCE
Tel: 33 (0) 5.61.28.51.14
Fax: 33 (0) 5.61.28.53.08
Email: tosser@coulouze.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at signasupport@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0024 row: b column: 23.

FEATURES

source

Location/Qualifiers
1..725
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="scan0024d.b.23"
/tissue_type="mixed"
/dev_stage="from embryos to adults"
/clone_lib="Sus Scrofa library (scan)"
/note="Tissues: adipose tissue, brain, kidney, liver,
muscle, ovary, testis, heart, hypothalamus, pancreas,
skin, spleen, thymus, placenta, pituitary gland, seminal
vesicle, small intestine, uterus, adrenals, bulbo urethral
gland, cerebral trunk, epididymis, female gonad,
gall-bladder, hippocampus, large intestine, male gonad,

```
ORIGIN
mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 630)
Normalizaton and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
8889548
COMMENT
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
clones from RESEARCH GENETICS. It should be noted that Bento Soares
is generating a small number of additional specialized
non-redundant arrays of BMAP cDNAs whose availability will be
considered under appropriate and limited collaborative arrangements
Seq primer: M13 forward
POLYA=No. Location/Qualifiers
1..630
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-CG0p-brq-g-09-0-UI"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NIH BMAP Ret4 S2"
/note="Vector: pT7T3D-pac (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI; The
NIH BMAP Ret4 S2 library is a subtracted library,
ultimately derived from mouse retina tissue libraries at
various stages of development. For a detailed description
of the library from which this clone was derived, please
visit our web site at brainest.eng.uiowa.edu. The tissue
for this library was contributed by Dr. Xin-Yuan Fu, Yale
University School of Medicine
TAG_SEQ=None found"

FEATURES
source
Alignment Scores:
Pred. No.: 7.39e-100 Length: 630
Score: 1069.50 Matches: 207
Percent Similarity: 99.52% Conservative: 1
Best Local Similarity: 99.04% Mismatches: 0
Query Match: 50.81% Indels: 1
DB: 2 Gaps: 1
US-09-939-483-5 (1-405) x BF467278 (1-630)
QY 87 ValIleThrIleGlyTyrGlyHisAlaAlaProSerThrAspGlyLysValPhe 106
Db 629 GTCATCACCATCCGCTATGTCATGCGGCCCGCAGCAGCGAGGAGGTGTTTC 570
QY 107 CysMetPheTyrAlaLeuLeuGlyTyrProLeuThrLeuIleMetPheGlnSerLeuGly 126
Db 569 TGCATGTTCTACGCGCTGCTGGCATCCCGCTCACACTAGTCATGTTCCAGAGCCTGGGT 510
QY 127 GluArgIleAsnThrPheValArgTyrLeuLeuHisArgAlaLysArgGlyLeuGlyMet 146
Db 509 GAACGCATCAACACCTCTCGTAGGTACCTGCTGCACCGTCCCAAGAGGGGCTGGGCATG 450
QY 147 ArgHisAlaGluValSerMetAlaAsnMetValLeuIleGlyPheValSerCysIleSer 166
Db 449 CGGCACGCCGAGGTGTCATGCGCAACATGGTGTCTCATCGGTTCGTGTCATCAGC 390

ORIGIN
melanocytes, stomach, udder"
Alignment Scores:
Pred. No.: 9.16e-103 Length: 725
Score: 1098.50 Matches: 216
Percent Similarity: 88.35% Conservative: 4
Best Local Similarity: 86.75% Mismatches: 20
Query Match: 52.19% Indels: 9
DB: 5 Gaps: 2
US-09-939-483-5 (1-405) x BX922107 (1-725)
QY 111 AlaLeuLeuGlyIleProLeuThrLeuIleMetPheGlnSerLeuGlyGluArgIleAsn 130
Db 2 CGCGCTCTGGGCATCCCGCTACGCTCGCTGTCATGTTCCAGAGCCTGGCGGAGCGATCAAC 61
QY 131 ThrPheValArgTyrLeuLeuHisArgAlaLysArgGlyLeuGlyMetArgHisAlaGlu 150
Db 62 ACCTTCTGGAAGTACCTGCTGCACCGCCCAAGAGGGGGCTGGGCATGCGCGCGCGAC 121
QY 151 ValSerMetAlaAsnMetValLeuIleGlyPheValSerCysIleSerThrLeuCysIle 170
Db 122 GTGTCCATGGCCACATGGTCTCATCGGCTTCTTCTCGTGCATTAGCAGCGCTGTGCATA 181
QY 171 GlyAlaAlaAlaPheSerTyrTyrGluArgTyrThrPhePheGlnAlaTyrTyrTyrCys 190
Db 182 GGCGCCCGCGCTTCTCTACTAGAGACTGGACCTTCTTCAGGCTCTACTACTACTGC 241
QY 191 PheIleThrLeuThrIleGlyPheGlyAspTyrValAlaLeuGlnLysAspGlnAla 210
Db 242 TTCAATCAGCTCACCATCGGCTTCGGCGACTACGTCGGCTGCAGAGGACCGGCG 301
QY 211 LeuGlnThrGlnProGlnTyrValAlaPheSerPheValTyrIleLeuThrGlyLeuThr 230
Db 302 CTGCAGACGCGCGCGAGTACGTGGCTTCTAGCTTCTGCTACATCTCTCAGCGGCTCACG 361
QY 231 ValIleGlyAlaPheLeuLeuValAlaLeuArgPheMetThrMetAsnAlaGluAsp 250
Db 362 GTCAATCGCGCTTCTGAACCTCGTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 421
QY 251 GluLysArgAspAlaGluHisArgAlaLeuLeuThrHisAsnGlyGlnAlaValGlyLeu 270
Db 422 GAGAAGCGCGAGCGCGAGCAGCGCGCTGCTCAGCGCAACGCGGCGGCGGCGGAGGC 481
QY 271 GlyGlyLeuSerCysLeuSerGlySerLeuGlyAspValArgProArgAspProValThr 290
Db 482 GCGCGCGCGGCTGCGCGGTGGCAGC-----CGCACACACCGAGACCGGCTCG 532
QY 291 CysAlaAlaAlaGlyGlyValGlyValGlyValGlySerGlyPheArgAsnVal 310
Db 533 TCCACGCGCGCGCGCGCG-----GGCGCGCGCGCTTCCGCAACGTC 574
QY 311 TyrAlaGluValLeuHisPheGlnSerMetCysSerCysLeuTyrTyrLysSerArgGlu 330
Db 575 TACGCCGAGGTGTCACCTTCCAGTCATGCTCGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 634
QY 331 LysLeuGlnTyrSerIleProMetIleProArgAspLeuSerThrSerAspThrCys 350
Db 635 AAGCTGAGTACTCATCCCCCATGATCATCCCGCGGACCTCTCCACGTCGCGACGCTGC 694
QY 351 ValGluHisSerHisSerSerProGly 359
Db 695 GTCAGCAGAGCCACTCTGTCGCCCGGG 721

RESULT 12
BF467278/c
LOCUS
DEFINITION UI-M-CG0p-brq-g-09-0-UI.s1 NIH BMAP Ret4 S2 Mus musculus cDNA clone
UI-M-CG0p-brq-g-09-0-UI 3', mRNA sequence.
ACCESSION BF467278
VERSION BF467278.1 GI:11536461
KEYWORDS EST.
```


Qy 167 ThrLeuCySilleGlyAlaAlaAlaPheSerTyTyTyGluArgTrpThrPhePheGlnAla 186
 Db 389 ACGCTGTGCATCGCGCGAGCTGCTTCTCTACTACGAGCGCTGGACTTTCTTCAGGCC 330
 Qy 187 TyTyTyTyTyCysPheIleThrLeuThrThrIleGlyPheGlyAspTyTyValAlaLeuGln 206
 Db 329 TATTACTACTGCTTCATCACCCTCACCACCATCGCTTCGGCGACTATGTGGCGCTGCAG 270
 Qy 207 LysAspGlnAlaLeuGlnThrGlnProGlnTyTyValAlaPheSerPheValTyIleLeu 226
 Db 269 AAGGACCGAGCGCTGCAGACCGCAGTATGTGGCTTCAGCTTCGTGTACATCCTC 210
 Qy 227 ThrGlyLeuThrValIleGlyAlaPheLeuAsnLeuValValLeuArgPheMetThrMet 246
 Db 209 ACGGGCTCACGGTCATCGCGGCTTCCTCAACCTCGTGGTGTGCTGCAGATTTCATGACCATG 150
 Qy 247 AsnAlaGluAspGluLeuArgAspAlaGluHisArgAlaLeuThrHisAsnGlyGln 266
 Db 149 AACGCCGAGGACGAGAGCGTGTATGCGGAGCACCAGCGCTTCATCGCACAACGGCCAG 90
 Qy 267 AlaValGlyLeuGlyGlyLeuSerCysLeuSerGlySerLeuGlyAsp---ValArgPro 285
 Db 89 GCTGTGGCTGGTGGCTGAGCTGCTGAGCGGTAGCTGGCGGCGGCGTGGCTGCC 30
 Qy 286 ArgAspProValThrCysAlaAlaAla 294
 Db 29 CGCGACCCAGTCACATCGCTCGGCC 3

RESULT 13
 BZ116659/c
 LOCUS
 DEFINITION BZ116659 665 bp DNA linear GSS 11-OCT-2002
 CH230-365B9.TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone.
 CH230-365B9, genomic survey sequence.
 BZ116659
 BZ116659.1 GI:23757606
 GSS.
 Rattus norvegicus (Norway rat)
 Rattus norvegicus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 665)
 Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K.,
 Shvartsbeyn,A., Gebregorgis,E., Overton,L., Russell,D., Chen,D.,
 Riggs,F., de Jong,P., and Fraser,C.M.
 Rat BAC End Sequences from Library CHORI-230 MboI segment
 Unpublished (1999)
 Other GSSs: CH230-365B9.TV
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the rat BAC library CHORI-230
 (http://www.chori.org/bacpac/rat230.htm). For BAC library
 availability, please contact Pieter de Jong (pjejong@mail.cho.org).
 Clones may be purchased from BACPAC Resources
 (http://www.chori.org/bacpac/or ering_information.htm). BAC end
 page: http://www.tigr.org/tldb/bac_ends/rat/bac_end_intro.html
 Plate: 365 row: B column: 9
 Seq primer: SP6
 Class: BAC ends.
 Location/Qualifiers
 1..665
 /organism="Rattus norvegicus"
 /mol_type="genomic DNA"
 /strain="BN/SnHsd/MCW"
 /db_xref="taxon:10116"
 /clone="CH230-365B9"
 /sex="Female"

/cell_type="Brain"
 /clone_lib="CHORI-230 Segment 2"
 /notes="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
 CHORI-230 Rat (BN/SnHsd/MCW) BAC library produced by
 Pieter de Jong"

ORIGIN
 Alignment Scores: 2,24e-98 Length: 665
 Pred. No.: 1055.50 Matches: 209
 Score: 97.67% Conservative: 1
 Percent Similarity: 97.21% Mismatches: 2
 Best Local Similarity: 50.14% Indels: 4
 Query Match: 8 Gaps: 2
 DB:

US-09-939-483-5 (1-405) x BZ116659 (1-665)

Qy 126 GlyGluArgIleAsnThrPheValArgTyTyLeuLeuHisArgAlaLysArgGlyLeuGly 145
 Db 645 GGTGAACGCATCAC-ACCTTCGTGAGGTACCTCTGCACCGTGCAGAGGGGGCTGGC 587
 Qy 146 MetArgHisAlaGluValSerMetAlaAsnMetValLeuIleGlyPheValSerCysIle 165
 Db 586 ATGGGCGACGCCAGGTGTCCATGGCCACATGGTGTCTCATCGGTTTCGTGTGATC 527
 Qy 166 SerThrLeuCySilleGlyAlaAlaAlaPheSerTyTyTyGluArgTrpThrPhePheGln 185
 Db 526 AGCAGCGTGTATCGCGCGCTGCTTCTCTACTATGAGCGCTGGACTTTCTTCCAG 467
 Qy 186 AlaTyTyTyTyCysPheIleThrLeuThrThrIleGlyPheGlyAspTyTyValAlaLeu 205
 Db 466 GCCTATTACTACTGCTTCATCACCTCACCACCATCGCTTCGGCGACTACGTGGCGCTG 407
 Qy 206 GlnLysAspGlnAlaLeuGlnThrGlnProGlnTyTyValAlaPheSerPheValTyIle 225
 Db 406 CAGAGGACCGAGCGCTGCNAACGACGCTCAGTACGTGGCTTCAGTTCGTATATATC 347
 Qy 226 LeuThrGlyLeuThrValIleGlyAlaPheLeuAsnLeuValValLeuArgPheMetThr 245
 Db 346 CTCACCGGCTCACGGTTCATCGCGGCTTCTCTCAACCTCGTGGTGTGCTGCATTCATGACC 287
 Qy 246 MetAsnAlaGluAspGluLysArgAspAlaGluHisArgAlaLeuThrHisAsnGly 265
 Db 286 ATGAACCGCGAGACGAGAGCGGTGTATGACAGACCGCTGCTGCTCAGCACAATGGC 227
 Qy 266 GlnAlaValGlyLeuGlyLeuSerCysLeuSerGlySerLeuGlyAsp---ValArg 284
 Db 226 CAGGCTGGCGGCTTGGTGGCTGAGCTGCCTAAGCGGTAGCTGGCGGATGGCGTGGT 167
 Qy 285 ProArgAspProValThrCysAlaAlaAlaAlaGly-----GlyValGlyValGlyVal 302
 Db 166 CCGCGGACCCAGTCACCTTGGCGAGCGGCTGCAGGCGGATGGCGGCTGGCGGCTC 107
 Qy 303 GlyGlySerGlyPheArgAsnValTyTyAlaGluValLeuHisPheGlnSerMetCysSer 322
 Db 106 GGTGGCAGCGGCTTCGCAACGCTATGCTGAAATGCTGCACCTTCAGTCCATGTGCTCG 47
 Qy 323 CysLeuTrpTyTyLysSerArgGluLysLeuGlnTyTySerIlePro 337
 Db 46 TGCCTGTGTACAGAGCCCGAGAGCTGCAGTACTCTCCATCCCC 2

RESULT 14
 BZ1745213
 LOCUS
 DEFINITION BZ1745213 892 bp mRNA linear EST 18-NOV-2003
 mRNA sequence.
 ACCESSION BZ1745213
 VERSION BZ1745213.1 GI:38417953
 KEYWORDS EST.
 SOURCE Xenopus tropicalis (western clawed frog)
 ORGANISM Xenopus tropicalis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

```

Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 892)
Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
Sanger Xenopus tropicalis EST project 2001 (11_2003)
Unpublished (2003)
Contact: Croning MDR
Sanger Institute
Hinnton, Cambridgeshire, CB10 1SA, UK
Email: tropesanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE ID: TtpA034e14.plkSP6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Nigel Garrett.
cDNA was oligo dT primed from 5ug of poly A+ RNA from tadpole
embryos. EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end.
Vector: pCS107; Site 1: EcoRI; Site 2: NotI
Host: Escherichia coli DH10B.
FEATURES
    source
        1..892
            /organism="Xenopus tropicalis"
            /mol_type="mRNA"
            /db_xref="taxon:8364"
            /clone="TtpA034e14"
            /dev_stage="tadpole (stage 35-40)"
            /lab_host="E. coli DH10B"
            /clone_lib="XGC-tadpole"
            /notes="vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from tadpole
embryos. EcoRI-NotI cut cDNA was then ligated into pCS107
with EcoRI at the 5' end and NotI at the 3' end"
ORIGIN
Alignment Scores:
Pred. No.:      4.57e-96      Length:      892
Score:          1035.00      Matches:    191
Percent Similarity: 87.12%      Conservative: 39
Best Local Similarity: 72.35%      Mismatches: 34
Query Match:     49.17%      Indels:     0
DB:              5          Gaps:          0
US-09-939-483-5 (1-405) x BX745213 (1-892)
QY  1  GluAsnValArgThrLeuAlaLeuValCysThrPheThrTyrLeuLeuValGlyAla 20
Db  22 CAGAAATGCGGTCTGTGTCCTCATTAATCTGCACATCTACCTTACCTGCTGGTGGCC 81
QY  21 AlaValPheAspAlaLeuGluSerGluProGluMetIleGluArgGlnArgLeuGluLeu 40
Db  82 GCGGTCTTTGACGCCCTGGAGTCCGACTACGATGAGGGAGGAGAGAGCTCAAGCC 141
QY  41 ArgGlnLeuGluLeuArgAlaAaGgTyrAsnLeuSerGluGlyTyrGluGluLeuGlu 60
Db  142 GAGGAGATACGGCTCAAGGGAAGTAGTCAACATCACCAGTCAGGACTACAGCAGCTGGAG 201
QY  61 ArgValValLeuArgLeuLysProHisLysAlaGlyValGlnTrpArgPheAlaGlySer 80
Db  202 CTGCTCATCATGACGTCAGGCACTTCACAGGGCTGGGGTTCAGTGGAAATTTGCTGCTCA 261
QY  81 PheTyrPheAlaIleThrValIleThrIleGlyTyrGlyHisAlaAlaProSerThr 100
Db  262 TTTTACTTTGCCATACTGTCTACTTACTTACTATAGGTACGACACGAGCTCCAGGAACT 321
QY  101 AspGlyGlyLysValPheCysMetPheTyrAlaLeuLeuGlyIleProLeuThrLeuLeu 120
Db  322 GATCGCGGAAGGCCCTTCTGCATGTTCTACGCCGTCTCTGGAATCCCACTCACTCTTGTG 381
QY  121 MetPheGlnSerLeuGlyGluArgIleAsnThrPheValArgTyrLeuLeuHisArgAla 140
Db  382 ATGTTCAGAGCTCTGGGAGCGCGATGAACCTTTGTCAAGTACCTCTCTGGAAGCGAATC 441
QY  141 LysArgGlyLeuGlyMetArgHisAlaGluValSerMetAlaAsnMetValLeuLeuGly 160
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
442 AGAATATGTTGGGATGCGGATGCGAGTACGAGCGTCTCCATGGAGAACATGTCACCGTTGCC 501
161 PheValSerCysIleSerThrLeuCysIleGlyAlaAlaAlaPheSerTyrTyrGluArg 180
502 TTCTTCTCTCGATCGGCACTCTTTGTCATCGGAGCGCGCTTCTCCCACTACGAAGAC 561
181 TtpThrPhePheGlnAlaTyrTyrCysPheIleThrLeuThrThrIleGlyPheGly 200
562 TGGAGTTTCTTTCAGTCCTATTATTACTGTTTATAACTTTTAACGACGATAGTTTCGGA 621
201 AspTyrValAlaLeuGlnLysAspGlnAlaLeuGlnThrGlnProGlnTyrValAlaPhe 220
622 GACTAGTGGCTCTGCAGAAACAGGCGCTTCAGAGAGAGCTCTCTACGTGGCTTTT 681
221 SerPheValTyrIleLeuThrGlyLeuThrValIleGlyAlaPheLeuAsnLeuValVal 240
682 AGCTTTATGTACATTTTAGTGGCTGACAGTATTATGGGCGCTTCTAAACTTAGTCGTT 741
241 LeuArgPheMetThrMetAsnAlaGluAspGluLysAtgAspAlaGluHisArgAlaLeu 260
742 CTCAGTTCTCTACTATGAACAGTGAAGAGGAGGAGCGGAGGAGCGGCGTCC 801
261 LeuThrHisAsn 264
802 TTGGCAGGAAC 813
RESULT 15
BF462825/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
BF462825 610 bp mRNA linear EST 04-DEC-2000
UI-M-CGOp-bni-a-11-0-UI-s1 NIH BMAP Ret4_S2 Mus musculus cDNA clone
UI-M-CGOp-bni-a-11-0-UI 3', mRNA sequence.
BF462825
BF462825.1 GI:11532008
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 610)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
889548
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
clones from RSEARCH GENETICS. It should be noted that Bento Soares
is generating a small number of additional specialized
non-redundant arrays of BMAP cDNAs whose availability will be
considered under appropriate and limited collaborative arrangements
Seq primer: M13 Forward
POLYA=No.
Location/Qualifiers
1..610
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-CGOp-bni-a-11-0-UI"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NIH BMAP Ret4_S2"
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The

```

NIH BMAP Ret4_S2 library is a subtracted library, ultimately derived from mouse retina tissue libraries at various stages of development. For a detailed description of the library from which this clone was derived, please visit our web site at braineset.eng.uiowa.edu. The tissue for this library was contributed by Dr. Xin-Yuan Fu, Yale University School of Medicine
TAG_SEQ=None found"

ORIGIN

Alignment Scores:

Pred. No.:	1 55e-95	Length:	610
Score:	1027.50	Matches:	199
Percent Similarity:	99.01%	Conservative:	1
Best Local Similarity:	98.51%	Mismatches:	1
Query Match:	48.81%	Indels:	1
DB:	2	Gaps:	1

US-09-939-483-5 (1-405) x BP462825 (1-610)

QY	94	GlyHisAlaAlaProSerThrAspGlyGlyLysValPheCysMetPheTyrAlaLeuLeu	113
DB	608	GGTCATGCGGCGCCAGCAGCAGGAGGCAAGGTGTTCTGCATGTTNTACGGCTGCTG	549
QY	114	GlyIleProLeuThrLeuIleMetPheGlnSerLeuGlyGluArgIleAsnThrPheVal	133
DB	548	GGCATCCCGCTCACATGATGTTCCAGAGCGCTGGGTGAACGATCAACACCTTCGTG	489
QY	134	ArgTyrLeuLeuHisArgAlaLysArgGlyLeuGlyMetArgHisAlaGluValSerMet	153
DB	488	AGGTACTGCTGTCACCGTGCAGAGGGGCTGGGATGCGGCACCGGAGGTGTCATG	429
QY	154	AlaAsnMetValLeuIleGlyPheValSerCysIleSerThrLeuCysIleGlyAlaAla	173
DB	428	GCCAAACATGCTCATCGGTTTCGTGTCGTCATCAGCAGCGCTGTGCATCGGCGCAGCT	369
QY	174	AlaPheSerTyrTyrGluArgTyrPhePheGlnAlaTyrTyrTyrCysPheIleThr	193
DB	368	GCCTTCTCTACTACGAGCGCTGAGCTTTCCTCCAGGCGCTATTACTACTGCTTCATCACC	309
QY	194	LeuThrThrIleGlyPheGlyAspTyrValAlaLeuGlnLysAspGlnAlaLeuGlnThr	213
DB	308	CTCACCAACATCGGCTTCGGCGACTATGTGGCGCTGCAGAGGACCGGCGCTGCAGACG	249
QY	214	GlnProGlnTyrValAlaPheSerPheValTyrIleLeuThrGlyLeuThrValIleGly	233
DB	248	CAGCCGCGATATGTGGCTTCAGCTTCGTGTACATCCTCAGCGGCGCTCAGGGTCATCGGC	189
QY	234	AlaPheLeuAsnLeuValValLeuArgPheMetThrMetAsnAlaGluAspGluLysArg	253
DB	188	GCCTTCTCAACCTCGTGTGGTGTGCGATTTCATGACCATGAACCGGAGGACGAGAACGCT	129
QY	254	AspAlaGluHisArgAlaLeuLeuThrHisAsnGlyGlnAlaValGlyLeuGlyGlyLeu	273
DB	128	GATCGGAGGACCGCGCCCTGCTCAGCAACACGGCAGGCTGTGCGGCTGGGTGGCCTG	69
QY	274	SerCysLeuSerGlySerLeuGlyAsp---ValArgProArgAspProValThrCysAla	292
DB	68	AGCTGCTGAGCGGTAGCTGCGCGACGCGGTGCGTCCCGCGACCCAGGTCAATCGGCT	9
QY	293	AlaAla 294	
DB	8	GCGGCC 3	

Search completed: September 16, 2005, 10:57:17
Job time : 4212 secs

This Page Blank (uspto)